T9519

STIC-Biotech/ChemLib

From:

Slobodyansky, Elizabeth

Sent:

Monday, September 13, 1999 5:22 PM

To:

STIC-Biotech/ChemLib

Subject:

09/068,507

This is a date case, please let me know if I need to do anything to facilitate.

Please search for case 09/068,507:

1. Seq ID NOs 1 + 2 against commercial and interference databases.

Thank you very much.

Elizabeth Slobodyansky





IMPORTANT INFORMATION ABOUT YOUR SEQUENCE SEARCH:

Compugen Sequence searching hardware and software explained:

This is the new sequence searching system that is currently being phased into as a replacement for the Maspar/Mpsrch platform. This system has been tested by both searchers and examiners, and has shown equivalent results to the Maspar system for the same databases. The results output format for all Compugen printed results are essentially the same except for translations.

Translation searching on Compugen explained:

The Compugen system utilizes Framesearch software for translations of proteins to nucleotides, and nucleotides to proteins. Some examiners have found these to be superior to the backtranslate software on Maspars.

FrameSearch searches a group of protein sequences for similarity to one or more nucleotide query sequences, or searches a group of nucleotide sequences for similarity to one or more protein query sequences. For each sequence comparison, the program finds an optimal alignment between the protein sequence and the corresponding codons on each the nucleotide sequence. Optimal alignments may include reading frame shifts. Please see any of the professional searching staff if you need assistance with this format.

File extensions for Compugen results transferred to floppy disks.

Compugen system search results will be delivered in one of two possible formats:

- 1. Standard concatenated files with .flp extension.
- Compressed .zip files which decompressed yield two files as described below:

US08123456.cmr - Contains all commercial databases, may include Issued
US08123456.pen - Contains pending file results only

VERY IMPORTANT NOTE ABOUT PENDING FILE SEARCHES.

If your search contains file names with the following bolded extensions:

US08123456.rap US08123456.rnp

Do not leave this search in the case, during prosecution, or after the case issues, since it contains pending data which is confidential.

QUESTIONS? Contact any of the following:

Dilip Pandya, Chief, Information Branch, 308-4268

Professional searching staff:

John Dantzman (308-4488); Jan Delaval (308-4498); Mary Hale (308-4258); Barb O'Bryen (308-4291); David Schreiber (308-4292); Paula Sheppard (308-4499); Mark Spencer (308-4266); Beverly Shears (308-4994); Alex Waclawiw (308-4491).

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FOR OFFICIAL USE ONLY 195-19 U.S. DEPARTMENT OF COMMERCE Patent and Trademark Office SEARCH REQUEST FORM Examiner # (Mandatory): Requester's Full Name: Art Unit _____ Location (Bldg/Room#): ____ /OD//_ Phone (circle 305 306 308)__ Serial Number: ___ Results Format Preferred (circle): PAPER DISK E-MAIL Title of Invention Inventors (please provide full names): Earliest Priority Date: _ Keywords (include any known synonyms registry numbers, explanation of initialisms): Search Topic: Please write detailed statement of the search topic, and the concept of the invention. Describe as specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples of relevant citations, authors, etc., if known. You may include a copy of the abstract and the broadcast or most relevant claim(s). FOR OFFICIAL USE ONLY STAFF USE ONLY Searcher: BOB Type of Search Vendors (include cost where applicable) . __/_ N.A. Sequence

_ A.A. Sequence

_ Structure (#)

_ Bibliographic

Litigation1

Procurement

Fulltext

_ Other

STN

_ Dialog

Dr. Link

Westlaw Other (specify)

__ Questel/Orbit

Lexis/Nexis

_ WWW/Internet

MP 2 In-house sequence systems (list)

PTO-1590 (2-99)

Searcher Location:

Date Picked Up:

Date Completed:

Clerical Prep Time:

Number of Databases:_

Terminal Time:

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非非常安全的人,我们也是我们的人,我们也是我们的人,我们的人,我们的人,我们的人,我们也不会有什么的,我们也不会有什么的,我们也不是我们的,我们的人,我们的人,我们们们的人,我们们们们的人,我们们们们		

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Sep 15 10:37:50 1999; MasPar time 11.18 Seconds 49.467 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: >US-09-068-507A-1 (1-26) from US09068507A.pep 199

Sequence: 1 KSSAYSLQMGATAIKQVKKLFKKWGW 26

Scoring table: PAM 150 Gap 15

Searched: 170751 seqs, 21266608 residues

Post processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 12:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 23:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 22.683; Variance 77.937; scale 0.291

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Query Match	Length	DB.	Ħ	Description	Pred. No.
1	199	100.0	26	24	W17989	Bacteriocin-inducing	2.87e-13
N	77	38.7	822	ü	W69847	Amino acid sequence o	4.40e+00
ω	75	37.7	793	29	W40117	Human GABA-BRla/b rec	6.84e+00
4	75	37.7	844	29	W40118	Rat GABA-BR1b recepto	6.84e+00
v	75	37.7	844	29	W40119	Human GABA-BR1b recep	6.84e+00
σ	75	37.7	960	29	W40116	Rat GABA-BRla recepto	6.84e+00
7	71	35.7	572	13	R78520	Partial ALK protein.	1.64e+01
æ	67	33.7	234	34	W62742	Streptococcus pneumon	3.87e+01
9	64	32.2	115	3	W28166	Staphylococcus aureus	7.28e+01
10	62	31.2	467	28	W41077	T. litoralis ADPHK pr	1.10e+02
11	62	31.2	572	œ	R39284	Parainfluenza virus t	1.10e+02
12	62	31.2	1577	16	R91047	Alpha-D-glucosyltrans	1.10e+02
13	60	30.2	13	24	W12897	Antimicrobial cationi	1.67e+02
14	60	30.2	74	18	R95262	Bacteriocin derivativ	1.67e+02
15	60	30.2	128	33	W61021	Streptococcus pneumon	1.67e+02
16	60	30.2	305	26	W23077	Sulfolobus solfataric	1.67e+02

;	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
	50	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	60	60	60	60	60	60
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	R3750	W3650	W3650	ス	R3419	R5666	R0664		R9813	W7326	R2402	R3890	L W37781	R9812	R9811		R9811	R9812	R9811	R9812		R9812		5 R31957		R0602		R790	9 P50501
	Ton ANC	e REN	Human RENT1 protein f	u8 antige	Sequence encoded by L	L-selectin.	—	lymphocyte		mphocyte h	Sequence of human lym				lymphocyte	lymphocyte			ᆸ	lymphocyte		G	cyte-specifi	a T	5	Viral haemagglutinin	Perdue strain of tran	I-3 haemagglutinin	Sequence of bovine pa
	040+0	.04e+0	2.04e+02	2.04e+02	. 04	2.04e+02		2.04e+02		.04e+0	.04e+0	.04e+0	.04e+0	.04e+0	.04e+0	.04e+0	.04e+0	.04e+0	2.04e+02	.04e+0	.04e+0	.04e+0			.67e+0	1.67e+02	61	7e+0	1.67e+02

ALIGNMENTS

8888888	88888	855555555555555555555555555555555555555	ק אפק אפק אפק אפק אפק אפק אפק אפק אפק אפ	RESULT ID W AC W AC W DT 1 DE B KW G KW V OS L PD 2
transformed with this vector, incorporated in the chromosome, and/or having integrated into its chromosome a promoter linked to an integrated gene encoding a specific protein are claimed. Typical applications are in fermentations (e.g. where the gene for an enzyme is regulated) and production of specific proteins, or where the bacteria express a surface antigen, as vaccines. Sequence 26 AA;	which are introduced into C11 cells can be induced by adding the (chemically synthesised) 26-residue inducing peptide. A recombinant vector containing such gene expression system, and host cells transformed with this worker is proposed to the observations.	Claim 5; Page 28; 39pp; English. This 26-residue peptide from Lactobacillus plantarum strain C11 can be used to induce and/or maintain the expression of genes involved in the production of bacteriocins. The invention relates to the discovery of a new regulatory mechanism for gene expression in lactic acid bacteria that includes previously unrecognised, strongly regulatable promoter elements (see T67142-48). Expression of other genes that are preceded by such promoter elements and	13-NOV-1995; NO-004575. (BRUK/) BRUKBERG M B. (EIJS/) ELISINK V G H. (RESI/) NESI F; Brurberg MB, Eijsink VGH, Nes IF; Brurberg MB, Eijsink VGH, Nes IF	UT 98 1 W17989; W17989; 10-DEC-1997 (first entry) Bacteriocin-inducing peptide. Gene expression; promoter; lactic acid bacterium; bacteriocin; vaccine; vector. Lactobacillus plantarum strain Cll. W09718316-Al. 22-MAY-1997.

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RESULT
ID WA
AC WA
DT 0:
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                                                                                                                                                                                                                                                                                                                                                 CC. The present sequence represents a p96 protein. This protein is present CC. the secretion associated 17s (SA-17s) complex. Eight proteins form the CC SA-17s complex, which binds a syntaxin-containing (SC) complex. The CS SA-17s polypeptides and nucleotide sequences encoding them can be used CC SA-17s polypeptides and nucleotide sequences encoding them can be used CC enhance binding for compounds which modulate vesticular release involved in CC synaptic transmission and other secretory processes. Compounds which CC enhance binding between the SA-17s and SC complexes may be used to treat CC an affective disorders such as depression, manic-depressive disorders and CC disease or Huntington's disease. Compounds which inhibit binding between the SA-17s and SC complexes may be used to treat a disorder of thought, Such as schizophrenia, or for anaesthesia. The compounds can also be used CC imbalances, the immune system for intervention in antigen processing, CC secreted immunomodulators, and viral processing, as well as CC enterpres and cC clidations, such as regulation of membrane trafficking CC currence and coll division.
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07-0CT-1998 (first entry)
Amino acid sequence of p96, a protein present in SA-17S complex.
Amino acid sequence of p96, a protein present in SA-17S;
p96 protein; secretion associated 17S complex; SC-17S;
syntaxin-containing complex; SC complex; screening; modulate;
vesicular release; synaptic transmission; secretory process;
treatment; affective disorder; depression; manic-depressive disorder;
treatment; affective disorder; depression; manic-depressive disorder;
anxiety disorder; neurodegenerative disease; schizophrenia; anaesthesia;
Human GABA-BRia/b receptor protein.

Gamma-animobutyric acid; GABA-BRia/b receptor; human; brain; agonist; inhibitory neurotransmitter; peripheral nervous system; antagonist; treatment; dementia; depression; anxiety; bronchial inflammation; ast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1d; Pages 107-109; 133pp; English.
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19-DEC-1997; U23498
                                                                              03-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neurodegenerative disease, hormone imbalances, immune system
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(STRD ) UNIV LELAND
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Similarity 100.0%;
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7; Misman
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Pred. No. 2.87e-13;
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This sequence represents a novel rat GABA-B receptor protein, GABA-BRIb. GABA (gamma-aminobutyric acid) is the major inhibitory neurotransmitter found in the brain and peripheral nervous system and this receptor may be used for the identification of GABA-B receptor agonists and antagonists. Such proteins may be used in treatment of dementia, depression, anxiety, epilepsy, spasticity, bronchial inflammation or asthma or to improve cognitive function. GABA-B receptor ligands and probes derived from this sequence can be used to assay for GABA-B receptors or DNA encoding them.
      Matches
                                  Query Match
Best Local :
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Bettler B, Bittiger H,
WPI; 98-042183/04.
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19-MAR-1997; E01370.
22-NOV-1996; US-756091.
30-MAY-1996; US-655716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gamma-animobutyric acid; GABA-BRIb receptor; rat; brain; agonist; inhibitory neurotransmitter; peripheral nervous system; antagonist; treatment; dementia; depression; anxiety; bronchial inflammation; a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W40118 standard; Protein; 844 AA. W40118;
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19-MAR-1997; E01370.
22-NOV-1996; US-756091.
30-MAY-1996; US-655716.
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98-042183/04.
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   37.7%;
larity 87.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Froestl W, Kaupmann K, Mickel
Score 75; DB 29; L
Pred. No. 6.84e+00;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 75; DB 29;
Pred. No. 6.84e+00;
0; Mismatches 1
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                                                        Length 844;
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19 KLFKKWGW 26

W40119 standard; Protein; 844 AA

03-JUN-1998 (first entry)

W40119;

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      purified GABA-B receptor or receptor protein - and antagonists of these which may be useful in treating nervous system disorders Claim 4; Page 86-90; 108pp; English.

This sequence represents a novel human GABA-B receptor protein, GABA-BRID. GABA (gamma-aminobutyric acid) is the major inhibitory neurotransmitter found in the brain and peripheral nervous system and this receptor may be used for the identification of GABA-B receptor agonists and antagonists. Such proteins may be used in treatment of dementia, depression, anxiety, epilepsy, spasticity, bronchial inflammation or asthma or to improve cognitive function. GABA-B receptor ligands and probes derived from this sequence can used to assay for GABA-B receptors or DNA encoding them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-DEC-1997.
19-MAR-1997; E01370.
19-MAR-1996; US-756091.
30-MAY-1996; US-655716.
(NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS AG.
WELLET B, Bittiger H, Froestl W, Kaupmann K, Mickel SJ;
WPI; 98-042183/04.
N-PSDB; V10267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human GABA-BRIb receptor protein.

Gamma-animobutyric acid; GABA-BRIa/b receptor; human; brain; agonist; inhibitory neurotransmitter; peripheral nervous system; antagonist; treatment; dementia; depression; anxiety; bronchial inflammation; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
WO9746675-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  epilepsy; cognitive function.
                                                                                                                                                                                                                                                                                                                                                                              03-JUN-1998 (first entry)
Rat GABA-BRLA receptor protein.
Gamma-animobutyric acid; GABA-BRLA receptor; rat; brain; agonist;
inhibitory neurotransmitter; peripheral nervous system; antagonist;
treatment; dementia; depression; anxiety; bronchial inflammation; asthma;
Claim 4; Page 50-56; 108pp; English.
This sequence represents a novel rat GABA-B receptor protein, GABA-BRIB. GABA (gamma-aminobutyric acid) is the major inhibitory neurotransmitter found in the brain and peripheral nervous system and this receptor may be used for the identification of GABA-B receptor agonists and antagonists. Such proteins may be used in treatment of dementia, depression, anxiety, epilepsy, spasticity,
                                                                                                                                                                                        (NOVS) NOVARTIS AG.
Bettler B, Bittiger H, Froestl W, Kaupmann K, Mickel WPI; 98-042183/04.
                                                                                                                                                                                                                                           11-DEC-1997.
19-MAR-1997; E01370.
22-NOV-1996; US-756091.
30-MAY-1996; US-555716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             w40116 standard; Protein; 960 AA.
w40116;
                                                                                                                                Purified GABA-B receptor or receptor protein - and antagonists these which may be useful in treating nervous system disorders
                                                                                                                                                                                                                                                                                                                                                              epilepsy; cognitive function.
                                                                                                                                                                          N-PSDB; V10264.
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Local Similarity 87.5%;
                                                                                                                                                                                                                                                                                                                                            norvegicus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 75; DB 29;
Pred. No. 6.84e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 844;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bronchial inflammation or asthma or to improve cognitive function GABA-B receptor ligands and probes derived from this sequence can used to assay for GABA-B receptors or DNA encoding them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; Q95541.

N-PSDB; Q95541.

Nethods for detecting human t(2;5) lymphoma - for detection and diagnosis of anaplastic large cell lymphoma(s) claim 21; Page 40-42; 70pp; English.

The translocation event that occurs in human t(2;5) lymphoma prings sequences from the nucleolar phosphoprotein (NPM) gene on chromosome 5q35 to those from a protein-tyrosine-kinase (ALK) gene on chromosome 2q23. Nucleic acids encoding a partial ALK protein conchromosome 2q23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-DEC-1994; U13947.
03-DEC-1993; US-160861.
(SJUD-) ST JUDE CHILDREN'S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALK protein; protein-tyrosine-kinase; fusion protein; NPM protein; nucleolar phosphoprotein; anaplastic large cell lymphoma;
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                                                                                                                       04-JUN-1998.
24-NOV-1997; U21976.
27-NOV-1996; US-031879.
                                                                                                                                                                                              Streptococcus pneumoniae polypeptide.
Polypeptide; ORF; open reading frame; infection; bacterial; streptococcal; bacteremia; diagnosis; prophylaxis.
                                                                                                                                                                                                                                              W62742 standard;
W62742;
09-NOV-1998 (fin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ribozymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (R78520) and the ALK/NPM fusion protein (R78521) were isolated (Q95541, Q95542). Identification of the NPM/ALK fusion allows lymphoma diagnosis, or therapy through the use of antisense RNA or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298 klfekwgw 305
            Streptococcus pneumoniae polynucleotides - useful for developing products for diagnosis, prevention and treatment of infections e
                                             Reid RH, Zarfos PN
WPI; 98-322654/28.
                                                           Black MT, Hodgson JE,
Reid RH, Zarfos PN;
                                                                                                                                                                                  Streptococcus pneumoniae.
                                                                                        (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                    WO9823631-A1.
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                                                                                                                                                                                                                                                                                                                                      6 SLQMGATAIKQVKKLFKKWGW
                                                                                                                                                                                                                                                                                                                                                                     2 slqegatgghscpqamkkwgw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 572 AA;
or diagnosis, prevention and treatment of infections bacteremia, meningitis or endocarditis
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                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                            Protein; 234 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                    35.7%;
                                                                          Knowles DJC,
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                     Score 71; DB 13; Le
Pred. No. 1.64e+01;
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                                                                             Lonetto MA, Nicholas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.84e+00
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                   e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a Staphylococcus aureus protein of unknown function. The DNA sequence was isolated from a library of clones of S. aureus WCUH 29 in Escherichia coli. The DNA sequence can be used in the construction of ribozymes and antisense sequences to control the expression of Staphylococcal genes. The DNA sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The present protein may be used to produce vaccines to enable a host to produce specific antibodies with antibacterial action. These vaccines and antibodies would protect
                              T. litoralis ADPHK protein sequence, SEQ ID NO 2. ADPHK; enzyme; hexokinase; hexose 6-phosphate; ac adenosine 2-phosphate; hexose.
Thermococcus litoralis. J09327297-A.
                                                                                                                        W41077 standard; Protein; 467
                                                                                                                                                                                                                                                                                                                                                                             a host against invasion by S. aureus, and conditions relating to Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled
                                                                                          05-MAY-1998
                                                                                                              W41077;
                                                                                                                                                                                                                                                                                                                                                                    skin syndrome,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Black MT, Burnham MK, Hodgson JE, Knowles DJC, Nicholas RO, Pratt JM, Reichard RW, Rosenberg M, Ward JM;
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21-AUG-1997; U02318.
19-FEB-1997; U02318.
20-FEB-1996; US-011888.
(SMIK) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus protein of unknown function.
Staphylococcus aureus protein; ribozyme; antisense sequence; control;
Staphylococcal gene; regulatory element; bacterial gene expression;
vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aureus infection
Claim 6; Page 507; 989pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 - used to isolate antimicrobial compounds, and in vaccines against S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 97-424969/39.
N-PSDB; T84091.
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The sequence is that of a Streptococcal polypeptide.

The polypeptide can potentially be used for the diagnosis and prevention of bacterial infections, especially SP infection.

It may be used for the treatment of diseases such as otitis media, conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleural empyema, endocarditis or infection of the cerebrospinal fluid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      toxic shock syndrome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W28166 standard; Protein; 115 AA.
                                                                                                                                                                                                                                      41 aldlkskdrdaikamfkkw 59
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                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ococcus aureus.
                                                                                                                                                                                                                                                                                                                                                  ome, and toxic shock syndrome.
                                                                                          (first entry)
                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                          32.2%;
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                                              hexose 6-phosphate; adenosine 1-phosphate;
                                                                                                                                                                                                                                                                   Score 64; DB 31;
Pred. No. 7.28e+01;
6; Mismatches 7
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Pred. No. 3.87e+01;
5; Mismatches 6;
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Best Local
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                                                                                                                                                                                                                                                                                                         Multimenta hybrid genes and their chimeric proteins - are vaccines against multiple pathogenic infections e.g. para-influenza virus and respiratory syncytial virus Claim 11; Figure 3A-3E; 80pp; English. A novel multimeric hybrid gene is used as a vaccine. The gene consists of two gene sequences which are linked and encode antigenic regions, these two sequences being derived from two different pathogens (parainfluenza virus (PIV) and respiratory syncitial virus (RSV)). The gene sequences that are particularly used are those which encode PIV-3 F and HN proteins (Q45683, Q45684) and RSV F and G proteins (Q45685, Q45686).
Alpha-D-glucosyltransferase; primer-independent; soluble glucan; sucrose; transgenic plant; cloning; Escherichia coll; phage lambda-Cl3; vector; plasmid pGSG501; plasmid pGSG502; gene transfer; crop improvement; storage carbohydrate; pasture;
                                                                 R91047 standard; Protein; 1577 AA.
R91047;
22-MAY-1996 (first entry)
Alpha-D-glucosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-JAN-1994 (first entry)
Parainfluenza virus type 3 (PIV-3) HN protein.
PIV; RSV; multimeric; hybrid; pathogen; chimer
                                                                                                                                                                                                                      432 lqlgiiditdysdirikwtw 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JAN-1993; CA0001.
06-JAN-1992; GB-000117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents a enzyme from T.litoralis, designated ADPHK, art is a hexokinase of the invention. The hexokinase of the invention is capable of catalysing the formation of hexose 6-phosphate and adenosine 1-phosphate from adenosine 2-phosphate and hexose. The new DNA sequence is used to transform the microorganism which is capable of producing a hexokinase. The recombinant microorganism is highly efficient at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; Q45684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ewasyshyn ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09314207-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R39284 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CONN-) CONNAUGHT LAB LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 production of enzyme
Claim 8; Page 14-16; 17pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA sequence encoding hexokinase - is used to transform organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ASAH ) ASAHI KASEI KOGYO KK. WPI; 98-104115/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-DEC-1997.
12-MAR-1997; 057330.
15-MAR-1996; JP-059136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 evrrylrewgw 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       producing the enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; V03981.
                                                                                                                                                                                                                                                         Local Similarity
nes 7; Conser
                                                                                                                                                                                       7 LOMGATAIKOVKKLFKKWGW 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 QVKKLFKKWGW 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93-243222/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fluenza virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         467 AA;
                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                     31.2%;
35.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    572 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Japanese.
                                                                                                                                                                                                                                                                     Score 62; DB 8;
Pred. No. 1.10e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 62; DB 28;
Pred. No. 1.10e+02;
5; Mismatches 2
                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chimeric protein; vaccine.
                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                                                                                                   Length 572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              readily digestible by ruminants
Claim 4; Page 16-20; 31pp; English.
Claim 5; Claim 6; Claim 6
and as a food preservative

Claim 3; Page 66; 89pp; English.

Chaim 3; Page 66; 80pp; English.

Chaim 3; Page 66; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-AUG-1995; AU0527.
24-AUG-1994; AU-007643.
(GIFF) GIFFARD P M.
(JACQ/) JACQUES N A.
(SIMP/) SIMPSON C L.
GIFFARD B. JACQUES NA,
WPI; 96-151376/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-MAR-1997.
23-AUG-1996; US-002687.
23-AUG-1995; US-002687.
(UYBR-) UNIV BRITISH COLUMBIA.
Falla TJ, Gough M, Hancock REW;
WPI; 97-179179/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antimicrobial cationic peptide CP-23.

Bacterial; viral; antitumour; food; preservative; inhibitor; growth; bacterium; yeast; endotoxaemia; sepsis; antibiotic; fungal; antiviral; Candida albicans; sterilant; Salmonella; Yersina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cationic peptide(s) having anti-microbial activity - used for the inhibition of bacterial and viral growth, as an antitumour agent,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W12897 standard; peptide; 13 AA. W12897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shigella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plants contg. new bacterial DNA encoding glucosyl transferase activity - retain higher levels of stored carbohydrate(s) in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               feedstuff; senescence; dextran; binder; food; pharmaceutical.
Streptococcus salivarius strain ATCC 25975.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                959 lagnaklfkewg 970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31.2%;
Local Similarity 66.7%;
es 8; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 IKQVKKLFKKWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1577 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                livestock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Simpson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 16;
1.10e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                 RESULT
                                                                                                                                                                   Query Match 30.2%;
Best Local Similarity 47.4%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
W61021 standa
W61021;
W61021;
13-OCT-1998
                                                                                                                                                                                                                                                               Protease(s) with highly specific cleavage activity - have proteolytic domains derived from N-terminus of ABC transporters, pref. 150 N-terminal amino acids of LagD Example 1; Figure 3C; 43pp; English.

Example 1; Figure 3C; 43pp; English.

Proteases derived from ABC-transporters containing N-terminal proteolytic domains are restriction proteases that can be used fo the cleavage of proteins at specific amino acid cleavage sites. To protease was produced by isolating a 5 kb Spel DNA fragment containing the protease N-terminal coding sequence, cloning this fragment into a pBluescript II SK+ plasmid and then using this fragment into a pBluescript II SK+ plasmid and then using the primers (T29648, T29649) to amplify the N-terminal proteolytic domain. The bacteriocin derivative was produced recombinantly as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiblotic resistant bacteria, combined with activity against the medically important fungus Candida albicans. In addition, the peptides are useful as antitumour agents and/or antiviral agents. The peptides may be used as sterilants or preservatives of materials susceptible to microbial or viral contamination, e.g. in processed foods to inhibit salmonella, Yersina and Shigella. The peptides are compact and tend to have a unique polyproline type II extended helix structure that permits them to span the membrane with relatively few amino acids. The peptides possess the ability to work synergistically with antibiotics, and in addition, some of then possess anti-endotoxin activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R95262;
11-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T 14
R95262 standard; Protein; 74 AA.
                                                                                                                                                                                                                                      test substrate for Sequence 74 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-1996.
16-NOV-1995; NO0213.
17-NOV-1994; NO-004411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protease; restriction protease; cleavage; proteolytic domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteriocin derivative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Havarstein LS, Ne
WPI; 96-268604/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HAVA/) HAVARSTEIN L S. (NESI/) NES I F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9616167-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lactococcus lactis.
                                                                                                                                   26 qmgrdlyddddkdpkkwgw 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 LFKKWGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ffkkwpw 7
                                                                                                     œ
                                 standard; Protein; 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
derivative (lactococcin G beta) peptide C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nes IF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Mature peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Enterokinase cleavage site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'label- N-terminal affinity tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
                                                                                                                                                                                                                                                    the ABC-protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30.2%;
                                                                                                                                                                   Score 60; D
Pred. No. 1.
1; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 60; DB 24;
Pred. No. 1.67e+02;
1; Mismatches 1
                                                                                                                                                                    Mismatches
                                                                                                                                                                                    DB 18;
1.67e+02;
                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 13
                                                                                                                                                                                                    Length
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                                                                                                                                                                   Gaps
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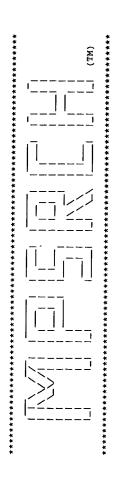
Streptococcus pneumoniae encoded polypeptide

(first entry)

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Search completed: Wed Sep 15 10:38:07 1999 Job time: 17 secs.
                                                                         Ś
                                                                                                             gb.
                                                                                                                                                                                                                      PT New isolated nucleic acids from Streptococcus pneumoniae - useful, preserved in the protein of meningitis anti-bacterial(s) for treatment and prevention of meningitis page 114; 130pp; English.

Claim 11; Page 114; 130pp; English.

CC The sequence is that of the polypeptide encoded by a region isolated crown s. pneumoniae. The protein, or agonists of it, can be useful as an antibacterial for treatment or prevention of infection, specifically caused by S. pneumoniae (particularly meningitis) but possibly also Helicobacter (pytori (ulcers and gastric cancer). It may be of particular use before insertion of an in-dwelling device or any other conversive procedure. The protein, or nucleic acid encoding cit, can also be used in vaccines to induce a cellular cand/or humoral immune response, or to screen for other antibacterials. The DNA may also contain flanking sequences that are potential sources of control elements for bacterial can be used diagnostically, e.g. to detect a mutation for serotyping or classifying infectious agents.
                                                                                                                                               Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAY-1998. U19226.
27-OCT-1997; U19226.
01-NOV-1996; US-029930.
(SMIK) SMITHKLINE BEECHAM CORP.
(SMIK) SMITHKLINE BEECHAM PLC.
Black MT, Hodgson JE, Knowles DJC, Lonetto MA, Nicholas RO, Reid RH, Zarfos PN;
WPI: 98-286586/25.
N-PSDB: V37409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pneumoniae. WO9819689-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coding region; ORF; open reading frame; antibacterial; infection; prevention; meningitis.
                                                                           14 IKQVKKLFKKWGW 26
                                                                                               60 ikaerdlfktw-w 71
|| : ||| | |
                                                                                                                                                 h 30.2%;
Similarity 53.8%;
7; Conservative
                                                                                                                                                 Score 60; DB 33; Le
Pred. No. 1.67e+02;
1; Mismatches 4;
                                                                                                                                                                                    Length 128;
                                                                                                                                                   Indels
                                                                                                                                                   1;
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Wed Sep 15 10:40:03 1999; MasPar time 1.59 Seconds 165.973 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-068-507A-1 (1-26) from US09068507A.pep 199

1 KSSAYSLQMGATAIKQVKKLFKKWGW 26 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

106580 seqs, 10152877 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-issued 1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1

Mean 21.296; Variance 76.695; scale 0.278 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ			SUMMARIES		
Result		Query		1	;	:	
2	acore	Match	match Length DB	3	d1	Description	Pred. No.
-	71	35.7	572	7	US-08-160-	Sequence 3, Applicatio	8.35e+00
2	71	35.7	1620	7	US-08-542-	~	8.35e+00
e	9	30.5	572	(4	US-08-185-	81,	8.17e+01
4	9	30.5	572	~	US-08-191-	81,	
S	29	29.6	231	7	US-08-808-	33,	
ø	29	29.6	316	'n	PCT-US95-0	2, 4	9.99e+01
7	29	29.6	316	~	US-08-464-	2,	9.99e+01
æ	53	29.6	372	4	5514582-2	Patent No. 5514582.	9.99e+01
σ	29	29.6	372	7	US-08-513-	Sequence 2, Applicatio	6
10	59	29.6	385	~	US-08-340-	~	ď
11	59	29.6	385	7	US-08-461-	7	9
12	28	29.1	410	7	us-08-073-	16,	Η.
13	57	28.6	49	7	US-08-456-	26,	Н
14	57	28.6	49	~	US-08-237-	26,	H
15	57	28.6	450	ო	PCT-US95-0	7, 4	1.49e+02
16	57	28.6	485	, -1	US-07-991-	42,	1.49e+02
17	57	28.6	544	Н	US-08-264-	۲,	1.49e+02
18	57	28.6	1167	, -	US-08-485-	φ	1.49e + 02
13	57	28.6	1167	7	US-08-290-	ý	1.49e+02
20	57	28.6	1168	-	us-08-620-	Sequence 9, Applicatio	1.49e+02
21	27	28.6	1220	-	US-08-158-	43,	1.49e + 02
22	57	28.6	1220	~	US-08-611-	Sequence 43, Applicati	1.49e+02
23	21	28.6	1289	4	5281530-3	Patent No. 5281530.	1.49e+02

35.7%; Score 71; DB 1; Length 572;

Query Match

24 57 28 6 1289 4 5426094 Patent No. 542609. 25 57 28 6 1289 1 105-09-15-5-5-5-5-5-5-5-5-5-5-5-5-5-5-5-5-5-5					XET
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24 57 28.6 1289 26 57 28.6 1289 28 57 28.6 1289 29 57 28.6 1289 31 57 28.6 1289 31 57 28.6 1289 33 57 28.6 1289 33 57 28.6 1289 33 57 28.6 1385 40 57 28.6 1385 40 57 28.6 1385 40 57 28.6 1385 40 57 28.6 1385 41 57 28.6 1385 41 57 28.6 1385 41 57 28.6 1385 41 57 28.6 1385 41 57 28.6 1385 41 57 28.6 1385 41 57 28.6 1385 41 57 28.6 1385 41 57 28.6 1385 41 57 28.6 1385 5	5426049-4 US-08-158- US-07-876- US-08-158- US-08-316- US-08-316- US-08-316- US-08-611- 5426049-1 US-08-611- US-08-108-0			08160861	PHAN W VEL FUSION SION PROTEI DETECTION 0 ESSLER, GOL K AVE NW SU disk Patible -DOS/MS-DOS 6-1880 #1.0 A: 1993 ION: T A 33217 ER: 656.0 MATION: -2678 : 35: 135
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SULY 4411 133 33 33 33 33 33 33 33 33 33 33 33		T.			3, App INFORM OF INV OF INV OF INV OF ENV OF SE OF SE
SULY 4411 133 33 33 33 33 33 33 33 33 33 33 33	00000000000000000000000000000000000000		XX	ø	TITLE
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Sequence 81, Application US/08185949B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 572 amino acids amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Morris, Stephan W.
APPLICANT: Look, A. Thomas
TITLE OF INVENTION: ALK Protein Tyrosine Kinase/Receptor and
TITLE OF INVENTION: Ligands Thereof
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: ALION New York Avenue, N.W., Suite 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/542,363
FILING DATE: 12-OCT 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fox, Samuel L.
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 0656.0400001/SLF/GKT
TELECHMONISCATION INFORMATION:
TELECHMONISCATION INFORMATION:
TELECHMONISCATION INFORMATION:
TELECHMONISCATION 125400
TELEFEAX: 202-371-2600
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Best Local Similarity 52.4%; Pred. No. 8.35e+00;
Matches 11; Conservative 1; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     572 AA.
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Pred. No. 8.35e+00;
1; Mismatches 9;
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MOLECULE TYPE: protein
SEQUENCE 1620 AA; 176416 MW; 13627521 CN;
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                                                                                                                                                                                                                                                                                                                                                            PRT;
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Patent No. 5770421
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08542363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 52.4%;
Matches 11; Conservative
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COUNTRY: US
ZIP: 20005
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US-08-542-363-2
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Sequence 81, Application US/08191866D
Patent No. 5783195
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D
APPLICANT: Macdonald, Richard D.
TITLE OF INVENTION: Recombinant Infectious Bovine
TITLE OF INVENTION: Rhinotrachetis Virus S-IBR-052 And Uses Thereof
NUMBER OF SEQUENCES: 99
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
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Sequence 81, Application US/08185949B
Patent No. 5874279
GENERAL INFORMATION:
APPLICANT: MAIN DOI:
TITLE OF INVENTION: Recombinant Infectious Bovine
TITLE OF INVENTION: About Contract and Infectious Bovine
TITLE OF INVENTION: About Contract and Infectious Bovine
TITLE OF INVENTION: About Contract and Infectious Bovine
TITLE OF INVENTION: PAPAGE AND TO THE Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: FORDAY
COMPUTER: IBM 330 466 DX2
COMPUTER: IBM 330 466 DX2
COMPUTER: DATACT RELEASE AND SECTION #1.25
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,949B
FILING DATE: U
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JENCE 572 AA; 64607 MW; 1762281 CN;
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Patent No. 5871992
GENERAL INFORMATION:
APPLICANT: Teebor, George W.
APPLICANT: Hibert, Timothy P.
TITLE OF INVENTION: MAMMALIAN ENDONUCLEASE III AND
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC USES THEREOF
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                            / Match 30.2%; Score 60; DB 2; Length 572; Local Similarity 30.0%; Pred. No. 8.17e+01; es 6; Conservative 6; Mismatches 8; Indels
          MORDING TYPE: Floppy disk
MORDING TYPE: Floppy disk
COMPUTER: IBM PC comparatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATE: US/08.191,866D
FILLING DATE: 4 February 1994
                                                                                                                                                                                                                                                                                                     231 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26.742
REFERENCE/DOCKET NUMBER: 1049-1-001 N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 572 AA; 64607 MW; 1762281 CN;
                                                                                                                                                                                                                                                                                                     PRT;
                                                            FILING DATE: 4 February 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 391-0525
TELEX: 42253
INFORMATION FOR SEQ ID NO: 81:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                       Sequence 33, Application US/08808550
                                                                                                                                                           i: 572 amino acids
amino acid
                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                   7 LOMGATAIKOVKKLFKKWGW 26
    COMPUTER READABLE FORM:
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STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                     US-08-808-550-33
                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                Query Match
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GENERAL INFORMATION:
APPLICANT: HG, ET AL.
TILLE OF INVENTION:
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                   Query Match 29.6%; Score 59; DB 2; Length 231; Best Local Similarity 45.5%; Pred. No. 9.99e+01; Matches 5; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: MS-DOS
SOTTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01827A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         325800-228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
JENCE 316.AA; 35444 MW; 517444 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application PC/TUS9501827A
                                                                                                                                                                                                                  NISM: S. cerevisiae
231 AA; 25982 MW; 264148 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGOR D.
REGISTRATION UNUMBER: 36,134
REFERRORE/DOCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 AMINO ACIDS
TYPE: AMINO ACID
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Concurrently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                        LENGTH: 231 amino acids TYPE: amino acids
                                                                                                                                       MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 6 BELLALICE CITY: ROSELAND STATE: NEW JERSEY
                                                                                                   single
                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: CC
                                                                                                                                                                                                                                                                                                                                                           161 HVHRLCKMWNW 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                16 QVKKLFKKWGW 26
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                                                                                                                                                                                                                        ORGANISM:
                                                                                                                        TOPOLOGY:
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1; Gaps
                                                                                                                                                                                                                Sequence 2, Application US/08464400
Patent No. 5786204
GENERAL INFORMATION:
APPLICANT: H. FT AL.
TITLE OF INVENTION: Human Prostatic Specific Reductase
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELA, BYRNE, BAIN, GILFILLAN,
STREET: 6 BECKER FARM ROAD
  Score 59; DB 3; Length 316;
Pred. No. 9.99e+01;
8; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.6%; Score 59; DB 2; Length 316; 28.0%; Pred. No. 9.99e+01; vative 8; Mismatches 9; Indels
                                                                                                                           316 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-228
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1704
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                     OCERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,400
FILING DATE: CONCURRENTLY
CLASSIFICATION 35
PRIOR APPLICATION DATA:
FILING APPLICATION DATA:
FILING APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                403 AA.
                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
JENCE 316 AA; 35444 MW; 517444 CN;
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                                                226 TIYSVHPGTVQSELVRHSSFMRWMW 250
                                                                                                                                                                                            Sequence 2, Application US/08464400
                                                                      3 SAYSLOMGATAIKOVKKL-FKKWGW 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     226 TTYSVHPGTVQSELVRHSSFMRWMW 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 SAYSLQMGATAIKQVKKL-FKKWGW 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 316 AMINO ACIDS TYPE: AMINO ACID
                                                                                                                        STANDARD;
Query Match
Best Local Similarity 28.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 29.6%;
Best Local Similarity 28.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                     CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
                                                                                                                    US-08-464-400-2
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ID 5514582-2
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                                                                                                           RESULT
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                                                              APPLICANT CARON, DANIEL J.; LASKY, LAURENCE A.
TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID IMMUGGLOBULINS
NUMBER OF SEQUENCES: 43
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,670
FILING DATE: 21-Jan-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 806,931
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: 808,031
FILING DATE: 16-DEC-1991
APPLICATION NUMBER: 808,031
FILING DATE: 12-NOV-1989
APPLICATION NUMBER: 315,015
FILING DATE: 23-FEB-1989
                                                                                                                                                                                                                                                                                                       Score 59; DB 4; Length 372;
Pred. No. 9.99e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: LASKY, LAURENCE A. APPLICANT: STACHELL, SCOTT E. APPLICANT: STACHELL, SCOTT E. APPLICANT: STACHELL, SCOTT E. APPLICANT: STONER, MARK S. APPLICANT: YEDNOCK, TED A. TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS CORRESPONDENCE ADDRESS: Genentech, Inc. STREET: 460 Point San Bruno Blvd CITY: South San Francisco CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patin (Geneticch)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,278
FILING DATE: 10-AUG-1995
CLASSIFICATION: 5530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/059027
FILING DATE: 06-MAY-1993
                                                                                                                                                                                                                                                                             403 AA; 45623 MW; 933915 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08513278
Patent No. 5840844
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 62.5%;
                                                                                                                                                                                                                                                                                                                               5; Conservative
                                 Patent No. 5514582.
                                                       Patent No. 5514582
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                                                                                                                                                                                                                                                       SEQ ID NO:2:
LENGTH: 372
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19 KLFKKWGW 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-513-278-2
           01-JAN-1900
                                                                                                                                                                                                                                                                             SEQUENCE
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Query Match
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Patent NO. 5808025
GENERAL INFORMATION:
APPLICANT: Tedder, Thomas F.
APPLICANT: Ransas, Geoffrey S.
TITLE OF INVENTION: CHIMBRIC SELECTINS AS SIMULTANBOUS
TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
UMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
APPLICATE OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 29.6%; Score 59; DB 2; Length 372; Best Local Similarity 62.5%; Pred. No. 9.99e+01; Antches 5; Conservative 2; Mismatches 1; Indels Matches 5; Conservative 2; Mismatches 3; Conservative 2; Mismatches 5; Conservative 2; Mismatches 5; Conservative 2; Mismatches 5; Conservative 2; Mismatches 5; Conservative 2; Mismatches 3; Conservative 2; Mismatches 3; Conservative 2; Mismatches 3; Conservative 2; Mismatches 3; Conservative 3; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: FLOPPY disk
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CORTWARE: PAREITIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,539A
APPLICATION NUMBER: 16-NOV-1994
CTASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          385 AA.
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NAME: 38,479
REGISTRATION NUMBER: 38,479
REFERENCE/DOCKET NUMBER: CG-104 CON
TELECOMUNICATION INFORMATION:
TELEPHONE: 212-596-9090
TELEPHONE: 212-596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/008,459
FILING DATE: 25-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                      ALTORAEL DEGGET, Ginger R.
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REGISTRATION NUMBER: 565D1C1
REFERENCE/DOCKET NUMBER: 565D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEPHONE: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        372 AA; 42209 MW; 729258 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08340539A
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                                    FILING DATE: 31-OCT-1552
PRIOR APPLICATION DATA:
07/315015
APPLICATION NUMBER: 07/786149
FILING DATE: 31-OCT-1991
                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHRRACTERISTICS: LENGTH: 372 amino acids TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                       FILING DATE: 23-FEB-1989
ATTORNEY/AGENT INFORMATION:
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CLASSIFICATION:
                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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Sequence 2, Application US/08461592B
Patent No. 5834410N
GENERAL INFORMATION:
APPLICANT: Tedder, Thomas F.
APPLICANT: Kansas, Geoffrey S.
TITLE OF INVENTION: GLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
SIREET: Ten Post Office Square
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                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 59; DB 2; Length 385;
Pred. No. 9.99e+01;
                                                                                                        Score 59; DB 2; Length 385;
Pred. No. 9.99e+01;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE. Patentin Release #1.0, Version #1.25
CURRAT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,592B
                                                                                                                                                                                                                                                                                       PRT; 385 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/ACTIVATION
MAME: James F. Haley, Jr.
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: CG-104
RELEGOMMUNICATION INPORMATION:
TELEPHONE: (212) 596-9090
TELEFA: 14-8367
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/008,459
FILING DATE: 25-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNMER: US 08/340,539
FILING DATE: 16-NOV-1994
FRING PAPLICATION DATA:
APPLICATION NUMBER: US 08/008,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
JENCE 385 AA; 43743 MW; 775024 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 385 AA; 43743 MW; 775024 CN;
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08461592B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 62.5%;
                                                                                                                                                                                                                                                                                               STANDARD;
                 : 385 amino acids
amino acid
3Y: linear
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                    y Match 29.6%;
Local Similarity 62.5%;
les 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                       JT 11
US-08-461-592B-2
                                                                                                                                                                                          29 NIFKLWGW 36
                                                                                                                                                                                                                            19 KLFKKWGW 26
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                        LENGIH:
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Matches

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Query Match
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                 RESULT
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            Gaps
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                                                                                                                   Sequence 16, Application US/08073807A
Patent No. 5646248
GENERAL INFORMATION:
APPLICANT: Sawada, Ritsuko
APPLICANT: Lowe, John B.
TILLE OF INVENTION: CELL SURFACE LAMP EXPRESSION
TITLE OF INVENTION: SELECTIN-DEPENDENT ADHESION
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 470 La Jolla Village Drive, Suite 700
    2; Mismatches 1; Indels
                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/073,807A
CIASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                        'Match 29.1%; Score 58; DB 1; Length 410; Local Similarity 28.6%; Pred. No. 1.22e+02; les 6; Conservative 5; Mismatches 10; Indels
                                                                    410 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 AA.
                                                                  PRT;
                                                                                                       Sequence 16, Application US/08073807A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
NCE 410 AA; 44988 MW; 908539 CN;
                                                                                                                                                                                                                                                                                                                      NAME: Cambell, Cathryn A. REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 9-L3
TELECOMMUNICATION INFORMATION:
TELEFAX: (619) 535-9091
INFORMATION FOR SEQ ID NO: SEQUENCE CHARATERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 26, Application US/08456647B
                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                          California
: United States
                                                                                                                                                                                                                                                                                                                                                                                       1: 410 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 SYALELNLTDSENATCLYAKW 46
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                                                   JT 12
US-08-073-807A-16
             29 NIFKLWGW 36
                           19 KLFKKWGW 26
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ZIP: 92122
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US-08-456-647B-26
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                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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Gaps
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Sequence 26, Application US/08456647B
Patent No. 5811516
GENERAL INFORMATION:
APPLICANT LEMBE Ph.D. et al., Greg E.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson p.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.6%; Score 57; DB 2; Length 49; 33.3%; Pred. No. 1.49e+02; vative 6; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 26, Application US/08237401A
Patent No. 5837448
GENERAL INFORMATION:
APPLICANT: Lemke Ph.D. et al., Greg E.
TITLE OF INVENTION: PROTEIN-TYROSINE KINASE GENES
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
CITY: La Jolla
                                                                                                                                                                                                                                                  SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,647B
FILING DATE: 02-JUN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                         FILING DATE: 02-TUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATE: 05-TO-100 DATE: 02-MAY-1994
FILING DATE: 02-MAY-1994
APPLICATION DATE: 05-MAY-1994
APPLICATION DATE: 05-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07251/007002
                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALLDIE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION UNMER: 31,678
REFERENCE/DOCKET NUMBER: 31,678
RELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
INFORMATION FOR SEQ ID NO: 26;
SEQUENCE HEARACTERSTSICS: 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LE TYPE: protein
49 AA; 5339 MW; 14108 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 26, Application US/08237401A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 KVSDFGLTKEASSTQDTGKLPVKW 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                               ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 33.3%;
nes 8; Conservative
                                                                                                             STREET: 4220 TIY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
OGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino a TOPOLOGY: lin MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-237-401A-26
                                                                                                                                                                    COUNTRY:
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STATE: C?
COUNTRY:
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Search completed: Wed Sep 15 10:40:11 1999
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APPLICANT: Sugen, Inc.
APPLICANT: Sugen, California 94063-4720
APPLICANT: Redwood City, California 94063-4720
APPLICANT: United States of America
APPLICANT: United States of America
APPLICANT: Hofgarten St. 2
APPLICANT: Munchen 80539
APPLICANT: Munchen 80539
APPLICANT: Munchen 80539
APPLICANT: Germany
TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 28.6%; Score 57; DB 2; Length 49;
Best Local Similarity 33.3%; Pred. No. 1.49e+02;
Matches 8; Conservative 6; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTE TEACH STATE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05008
                    COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC Compatible
COMPUTER: TBM PC COMPATION
OFFWARE: PatentIn Release #1.0, Version #1.25
SOFFWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/237,401A
APPLICATION NUMBER: US/08/237,401A
RPLICATION NUMBER: US/08/237,401A
APPLICATION NUMBER: US/08/237,401A
APPLICATION NUMBER: US/08/237,401A
RPLING DATE: 15-MAY-1992
ATTORNEY/AGENT INFONATION:
NAME: Halle Ph.D. Lisa A.
REGISTRATION NUMBER: 33,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     450 AA.
                                                                                                                                                                                                                                            07251/007001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                       REFERENCE, DOCKET WIMBER: 07251
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5070
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
JENCE 49 AA; 5339 MW; 14108 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 KVSDFGLTKEASSTQDTGKLPVKW 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                    LENGTH: 49 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: New York
TRY: U.S.A.
10036
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STATE: Ne
COUNTRY:
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PCT-US95-05008-7
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                                                  PRIOR APPLICATION DATA

APPLICATION NUMBER: US
FILING DATE: 22-APR-1994
CLASSIFFACTION:
AUTORNEY, AGENT INFORMATION:
NAME: COTUZZI, LAUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-074
REFERENCE/DOCKET NUMBER: 7683-074
TELECOMMUNICATION INFORMATION:
TELEFONAM: (212)869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 mming acids
                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE 450 AA; 50704 MW; 1071733 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     329 KVSDFGLTKEASSTQDTGKLPVKW 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 24-APR-1995
                                                                                                                                                                                                                                                                                                                                                                          unknown
                     CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: unh
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm Wed Sep 15 10:38:24 1999; MasPar time 4.14 Seconds 251.685 Million cell updates/sec

Tabular output not generated.

>US-09-068-507A-1 (1-26) from US09068507A.pep 199 Description: Perfect Score: Sequence:

1 KSSAYSLQMGATAIKQVKKLFKKWGW 26

PAM 150 Gap 15 Scoring table:

122810 segs, 40068593 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Mean 31.155; Variance 49.460; scale 0.630 pir60 1:pir1 2:pir2 3:pir3 4:pir4

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	5.88e-20	7.06e-02	1.56e-01	2.30e-01	2.30e-01	1.55e+00	2.25e+00	3.25e+00	3.25e+00	3.25e+00	4.68e+00	001009	00-100	6.70e+00	6.70e+00	6.70e+00	9.58e+00	1.36e+01	1.366+01	1.93e+01	1.93e+01	1.93e+01	1 930+01	10000	T. SSETOT
	Description	plantaricin A - Lacto	probable membrane pro		hypothetical protein	gamma-aminobutyric ac	virC-region hypothet1	bo-type ubiguinol oxi	dedA protein - Mycoba	hypothetical protein	gene 38 protein - pha	himothetical protein		hypothetical protein	conserved hypothetica	cerebrin-50 - human	NAD+ ADP-ribosyltrans	creatine kinase (EC 2	transcription regulat	hypothetical protein	conserved hypothetica	reverse transcriptase	enolase (eno) homolog	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	4	lanosterol 14aipna-ue
	GI .		525345	A42420	571021	JE0356	A40361	B38129	572727	C71060	241185	100000000000000000000000000000000000000	231730	A71174	F69771	I52374	S42208	A27708	139841	F71638	C70221	DH0217	10000	1000	24.2389	JC4240
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o a	_	83.4	. 0		200	27.7	35.2	34.7	3.4.2			34.2	33.7	33.7	33.2	33.2	33.7	32.7	32.2	32.2	31.7			7.10	31.7	31.7
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probable RNA-directed hypothetical protein probable RNA-directed ribosomal protein S3 major capsid protein hypothetical protein hypothetical protein heat shock transcript heat shock transcript heat shock transcript heat shock transcript hemagglutinin-neurami hemagglutinin neurami hemag
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44444444444444444444444444444444444444

ALIGNMENTS

1 A45913 #type complete plantaricin A - Lactobacillus plantarum plantaricin A - Lactobacillus plantarum #formal_name Lactobacillus plantarum 14-May-1993 #text_change 12-Sep-1997 A45913 NNE A45913 NNE A45913 NNSSen-Mayer, J.; Granly-Larsen, A.; Sletten, K.; Daeschel, M.; Nes, I.F. Dmission A45913 M.; Nes, I.F. M.; Nes, I.F. M.; Nes, I.F. M.; Daeschel,	Query Match 83.4%; Score 166; DB 2; Length 22; Best Local Similarity 100.0%; Pred. No. 5.88e-20; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 AVELONGADATEONEMI 22
es es	h Similari 22; Con	TATACAST
RESULT 1 ENTRY TITLE ORGANISM DATE ACCESSIONS REFERENCE #authors #submission #secession #sectatus ##sterides KEYWORDS SUMMARY	Query Match Best Local 9 Matches	144

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\$25345 #type complete probable membrane protein YCR089w - yeast (Saccharomyces cerevisiae)	hypothetical protein YCR1102 #formal_name Saccharomyces cerevisiae 30-sep-1993 #sequence_revision 30-Sep-1993 #text_change 06-Feb-1998	ESSIONS S25345; S19504 BERNCE S2545 #authors Wilson, C.; Grisanti, P.; Frontali, L. #authors Vasst (1992) 8:569-575 #fjurnal The complete sequence of a 6146 bp fragment of Saccharomyces #fitle cerevisiae chromosome III contains two new open reading frames. #cross-references WUID:92397594 #accession S25345	##molecule_type DNA ##residues 1-1609 ##label WIL ##cross-references GB:X59720; EMBL:S43845; NID:g1907116; PID:e264634;
RESULT 2	ALTERNATE_NAMES	ACCESSIONS REFERENCE #authors #journal #title #cross-refere #accession	##molecule_t
ENTRY	ORGANISM		##residues
TITLE	DATE		##cross-refe

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##residues 1-1609 ##label FRO
##cross-references EMBL:X59720; NID:91907116; PID:e264634; PID:91907227;
MIPS:YCR089w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stoltzfus, L.J.; Sosa-Pineda, B.; Moskowitz, S.M.; Menon, K.P.; Dlott, B.; Hooper, L.; Teplow, D.B.; Shull, R.M.; Neufeld, E.F.
                                                                                                                                                                                                                                                                                                         #domain transmembrane #status predicted #label TMI\
#domain transmembrane #status predicted #label TMZ
#length 1609 #molecular-weight 166047 #checksum 8346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A42420 #type complete
L-iduronidase (EC 3.2.1.76) - dog
#formal_name Canis lupus familiaris #common_name dog
17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence extracted from NCBI backbone (NCBIP:89830)
                                     Frontali, L.; Grisanti, P. submitted to the Protein Sequence Database, March 1992 819504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D71021 #type complete
hypothetical protein PH1465 - Pyrococcus horikoshii
#formal_name Pyrococcus horikoshii
14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #journal J. Biol. Chem. (1992) 267:6570-6575
#title Cloning and characterization of cDNA encoding canine alpha-L-iduronidase. mRNA deficiency in mucopolysaccharidosis I dog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #Superfamily L-iduronidase
glycosidase; hydrolase; polysaccharide degradation
#length 655 #molecular-weight 72939 #checksum 4797
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Pred. No. 7.06e-02;
8; Mismatches 7; Indels
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Pred. No. 1.56e-01;
8; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##residues 1-655 ##label STO
##cross-references GB:M81893; NID:g163963; PID:g163964
##experimental_source testis
                                                                                                                                                                                              ##CICSS_references SGD:S0000685; MIPS:YCR089w#map_position 3R
                                                                                                                                                                                                                                                               transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1092 PSQYSLSTATTTINGIKTVYTTW 1114
PID:91907227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267 SSIXILEQEQATVQQIRRLFPKFA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 SSAYSLOMGATAIKQVKKLFKKW 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preliminary
                                                                                                                                                                                                                                                                                                                                                                                          Match 39.2%;
Local Similarity 34.8%;
es 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38.28;
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                                                                                                ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##molecule_type mRNA
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                                                        #submission
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                                                                              #accession
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                  #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
#authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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##cross-references GB:AP000006; NID:g3236133; PID:d1031515; PID:g3257889
##experimental_source strain OT3
##note this accession replaces an interim accession for a sequence replaced by GenBank
Hino, Y.; Yamamoto, S.; Sekine, M.; Baba, S.; Kosugi, H.; Hosoyama, A.; Nagai, Y.; Sakai, M.; Ogura, K.; Otsuka, R.; Nakazawa, H.; Takamiya, M.; Ohituk, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, A.; Aoki, K.; Yoshizawa, T.; Nakamura, Y.; Robb, F.T.; DNA Res. (1998) 5:55-76 Complete sequence and gene organization of the genome of a hyper-thermophilic archaebacterium, Pyrococcus horikoshii
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Blochem. Blophys. Res. Commun. (1998) 250:240:245
GABA (gamma-amino-butyric acid) neurotransmission:
Identification and fine mapping of the human GABAb receptor
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#product gamma-aminobutyric acid receptor B #status
predicted #label MAT\
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#formal_name Homo sapiens #common_name man
05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change
12-Feb-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preliminary; nucleic acid sequence not shown;
translation not shown
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Pred. No. 2.30e-01;
...marches 2; Indels
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#accession JE0356
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Local Similarity 58.3%;
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23,83,439,481,501,
513,630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytochrome aa3 quinol oxidase chain I; quinol oxidase aa3-600 #formal_name Bacillus subtilis 15-0ct-1994 #text_change 04-mr-1993 #sequence_revision 15-0ct-1994 #text_change
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                                                                                                                                                                                                                                                                                                                                                                   #authors Michiels, T.; Vancotegham, J.C.; Lambert de Rouvroit, C.; China, B.; Gustin, A.; Boudry, P.; Cornelis, G.R. T.; Durnal J. Bacteriol. (1991) 173:4994-5009 at the secretion of Yop #title hanlysis of virC, an operon involved in the secretion of Yop proteins by Yersinia enterocolitica.
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##cross-references GB:M86548; NID:9143395; PID:9143397
##note sequence extracted from NCBI backbone (NCBIN:103632,
##note NCBIP:103603)
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virC-region hypothetical protein yscA - Yersinia
virC-region hypothetical plasmid pry
enterocolitica plasmid pry
#formal_name Yersinia enterocolitica
21-Feb-1992 #sequence_revision 21-Feb-1992 #text_change
                                                                              Gaps
#length 960 #molecular-weight 108148 #checksum 3766
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#length 32 #molecular-weight 3815 #checksum 9835
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                                       y Match 37.7%; Score 75; DB 2; Length 960; Local Similarity 87.5%; Pred. No. 2.30e-01; Indels nes 7; Conservative 0; Mismatches 1; Indels
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Pred. No. 1.55e+00;
6; Mismatches 5;
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Guery Match
Best Local Similarity 31.3%;
Matches 5; Conservative
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Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.W.;
Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessateres, P.;
Alloni, A.; Borchert, S.; Boriss, R.; Boursier, L.; Brans,
Bolotin, A.; Bergnell, S.C.; Bron, S.; Brouillet, S.;
A.; Braun, M.; Brignell, S.C.; Bron, S.;
Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
Codani, J.J.; Connerton, I.F.; Cummings, N.J.;
Choi, S.W.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.;
Choi, S.W.; Demisor, F.; Devine, K.W.; Dusterhoeft, A.;
Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.;
Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.;
Ellist, Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fullita,
Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fullita,
S.Y.; Glaser, Y.; Fuma, S.; Gallzzi, A.; Gallelon, N.; Ghim,
K.; Hand, Y.; Haper, M.; Golightly, E.J.; Grandi,
G.X.; Glaser, Y.; Klaerr-Blanchard, M.; Klaer, B.; Karamata, D.;
Kuilta, K.; Lapidus, A.; Holsappel, S.; Hosono, S.;
Kuilta, K.; Lapidus, A.; Lardinois, S.; Lauber, J.;
Kuilta, K.; Lapidus, A.; Lardinois, S.; Lauber, J.;
Kuilta, K.; Lapidus, A.; Lavinos, M.; Noone, D.; O'Railly,
M.; Woestl, D.; Nakai, S.; Nedine, M.; Park, S.; Prescott,
W.; Pohl, T.M.; Portetelle, D.; Porwollk, S.; Prescott,
W.; Pohl, T.M.; Portetelle, D.; Porwollk, S.; Scanlon,
B.; Scorchi, A.; Serror, S.; Schfone, E.; Sekkuott, A.; Serror, S.; Schroch, S.; Schroch, M.; Takaula, A.; Damakoshi, A.; Takaunoth, M.; Takaunoth, M.; Takaunoth, M.; Takaunoth, M.; Takanatu, K.; Takaunoth, M.; Tamakoshi, A.; Takaunoth, M.; Takaunoth, M.; Takaunoth, M.; Vanider, E.; Vassaroctti, M.; Vasumoto, M.; Vasumoto
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#domain cytochrome-c oxidase chain I homology #label
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#title Bacillus subtilis genome project: cloning and sequencing of the 97 kb region from 325 degrees to 333 degrees.
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                                                                                                                                                                      ##molecule_type DNA
##residues
#scsidues
##coss-references EMBL:X73124; NID:g413923; PID:g413962
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Nature (1997) 390:249-256
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#domain transmembrane #status predicted #label TM8\
#domain transmembrane #status predicted #label TM9\
#domain transmembrane #status predicted #label TM10\
#domain transmembrane #status predicted #label TM10\
#domain transmembrane #status predicted #label TM11\
#binding_site heme a iron (His) (axial ligands) #status
#binding_site copper (His) #status predicted\
#binding_site heme a iron (His) (axial ligands) #status
#binding_site heme a3 iron (His) (axial ligand) #status
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Hino, Y.; Yamamoto, S.; Sekine, M.; Baba, S.; Kosugi, H.;
Nakazawa, A.; Nagai, Y.; Sakai, M.; Ogura, K.; Otsuka, R.;
Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Otsuka, R.;
A.; Aoki, K.; Yoshizawa, T.; Nakamura, Y.; Robb, F.T.;
DNA Res. (1998) 5:55-76
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        dedA protein - Mycobacterium leprae
B1177_C2_172 protein
19-Mar_197_*sequence_revision 25-Apr-1997 *text_change
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hypothetical protein PH1177 - Pyrococcus horikoshii
#formal_name Pyrococcus horikoshii
14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change
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                                                                                                                                                                                 #length 649 #molecular-weight 73838 #checksum 999
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Pred. No. 2.25e+00;
4; Mismatches 8; Indels
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1-134 ##label SMI
##cross-references EMBL:U00011; NID:9466807; PID:9466816
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34.2%; Score 68; DB 2; Length 134;
Best Local Similarity 28.6%; Pred. No. 3.25e+00;
Matches 6; Conservative 8; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                 91 FPKHFGPGHVALVERLFNRWG 111
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##residues 1-1
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102,417
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Analysis of cis and trans acting elements regulred for the lattiation of DNA replication in the Bacillus subtilis #cross-references MulD:94172631
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                               gene 38 protein - phage SPP1
#formal_name phage SPP1
20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
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                                                                                                                                                                #length 157 #molecular-weight 18430 #checksum 3665
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Yeast (1993) 9:351-361
Molecular genetics in Saccharomyces kluyveri: the HIS3
homolog and its use as a selectable marker gene in S.
kluyveri and Saccharomyces cerevisiae.
     preliminary; nucleic acid sequence not shown; translation not shown
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# length 256 #molecular-weight 29998 #checksum 6866
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34.2%; Score 68; DB 2; Length 157;
Best Local Similarity 30.0%; Pred. No. 3.25e+00;
Matches 6; Conservative 7; Mismatches 7; Indels
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Pred. No. 3.25e+00;
4; Mismatches 4; Indels
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33.7%; Score 67; DB 2; Length 341;
Matches 6; Conservative 5; Mismatche.
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#length 341 #checksum 822
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##molecule_type DNA
##residues 1-256 ##label PE2
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Matches 5; Conservative
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                              ##molecule_type DNA
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Kanst, F.; Ogasawara, N.; Bertero, M.G.; Bessleres, P.;
Kanloni, G.; Azevedo, V.; Bertero, M.G.; Bessleres, L.; Brans, Bolotlin, A.; Bercheri, S.; Bronis, S.; Brouillet, S.; Brouillet, S.; Brouillet, S.; Brouillet, S.; Bronis, S.; Bronis, S.; Bronis, S.; Bronis, S.; Calawell, B.; Caphano, V.; Carter, N.M.; Daniel, R.A.; Delizot, F.; Devine, K.D.; Esterofeth, Daniel, R.A.; Denizot, F.; Devine, K.D.; Eritz, C.; Fultz, E.; Entlan, K.D.; Eritz, C.; Fultz, A.; Entlan, K.D.; Eritz, C.; Fultz, C
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Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Hosuya, H.
Hino, Y.; Yammamoto, S.; Sekine, M.; Ogura, K.; Otsuka, R.;
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Nakazawa, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,
A.; Aoki, K.; Yoshizawa, T.; Nakamira, Y.; Robb, F.T.;
Horikoshi, K.; Masuchi, Y.; Shizuya, H.; Kikuchi, H.
Horikoshi, K.; Masuchi, Y.; Shizuya, H.; Kikuchi, H.
Complete Sequence and gene organization of the genome of a complete Sequence and gene organization of the genome of a hyper-thermophilic archaebacterium, Pyrococcus horikoshii
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hypothetical protein PH0589 - Pyrococcus horikoshii
#formal_mame Pyrococcus horikoshii
#formal_mame Pyrococcus horikoshii
14-Aug_1998 #text_change
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#length 457 #molecular-weight 52090 #checksum 429
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M.; Mogawa, K.; Ogivara, S.; Noback, M.; Noone, D.; O'Rellly,
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Schheich, S.; Schoeter, R.; Scoffone, E.; Sekiguch, J.;
Schowska, M.; Seror, S.J.; Parada, T.; Takahashi, H.;
Schowska, M.; Tacconi, E.; Takahashi, H.;
B.; Sorokin, A.; Tacconi, E.; Takahashi, H.;
B.; Sorokin, A.; Tacconi, E.; Takahashi, H.;
Takamatur, K.; Takahani, M.; Tamakoshi, A.; Tanakoshi, A.; Tanakoshi, A.; Tanakoshi, A.; Tanakoshi, A.; Tanakoshi, M.; Tanakoshi, M.; Tanakoshi, M.; Tanakoshi, A.; Tanakoshi, M.; Tanakoshi, A.; Tanakoshi, M.; Tanakoshi, A.; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #authors Li, A.H.; Silvestrini, B.; Leone, M.G.; Giacomelli, S.; Cheng, C.Y.
#journal cheng, C.Y. Biol. Int. (1995) 35:135-144
Correction-50, a human cerebrospinal fluid protein whose mRNA #title is present in multiple tissues but predominantly expressed in the lymphoblastoid cells and the brain.
#cross-references MUID:95253026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##residues 1-246 ##label KUN ##residues 1-246 ##label KUN ##residues ##cross-references GB:299106; GB:AL009126; NID:92632653; PID:e1182416; ##cross-references GB:299106; GB:AL009126; NID:92632653; PID:e1182416; ##cross-references GB:299106; GB:AL009126; NID:92632653; PID:e1182416; ##cross-references GB:209106; GB:AL009126; NID:92632653; PID:e1182416; ##experimental_source strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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02-Jul-1996 #text_change
02-Jul-1996 #sequence_revision 02-Jul-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #length 246 #molecular-weight 27786 #checksum 1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.2%; Score 66; DB 2; Length 435; Best Local Similarity 41.7%; Pred. No. 6.70e+00; Matches 10; Conservative 4; Mismatches 10; Indels Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 246;
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Pred. No. 6.70e+00;
6; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.2%;
Iocal Similarity 52.9%;
les 9; Conservative
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S42208
Masutani, M.: Nozaki, T.; Hitomi, Y.; Ikejima, M.; Nagasaki,
K.; de Prati, A.C.; Kurata, S.; Natori, S.; Sugimura, T.;
Esumi, T.: 1904, 200.607-614
                                                                                                                                                                                                                                     #domain DNA binding #status predicted #label DNA\
#domain auto-modification #status predicted #label ANO\
#domain NAD binding #status predicted #label ANO\
#length 996 #molecular-weight il3018 #checksum 1061
             S42208 #type complete
NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - flesh fly
pol(sarcophaga peregrina)
#formal_name Sarcophaga peregrina
06.Feb-1995 #sequence_revision 06.Feb-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
33.2%; Score 66; DB 2; Length 996;
Best Local Similarity 34.6%; Pred. No. 6.70e+00;
Matches 9; Conservative 7; Mismatches 10; Indels 0; Gaps
                                                                                                                                                                                   #journal Eur. J. Blochem. (1994) 220:607-614
Cloning and functional expression of poly(ADP-ribose)
#cross-references MID:94170813 from Sarcophaga peregrina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: Wed Sep 15 10:38:41 1999
Job time : 17 secs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  552 KNSFYKLOLLESDMKNRFWVFRSWGR 577
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                                                                                                                                                                                                                                                                                                                                    ##residues
CLASSIFICATION
KEYWORDS
15
                                                                                                         ACCESSIONS
REFERENCE
                                                                                                                                            #authors
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DATE
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370-507
508-996
SUMMARY
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Sep 15 10:38:57 1999; MasPar time 3.11 Seconds 236.414 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-068-507A-1 (1-26) from US09068507A.pep 199

Description: Perfect Score: Title:

1 KSSAYSLQMGATAIKQVKKLFKKWGW 26 Sequence:

Scoring table:

77977 seqs, 28268293 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

swiss-prot37 1:swissprot

Mean 31.897; Variance 43.884; scale 0.727 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Pred. No.	5.90e-32	1.20e-02	2.93e-02	3.91e-01	5.93e-01	8.97e-01	1.35e+00	1.35e+00	2.02e+00	3.02e+00	4.48e+00	6.62e+00	9.73e+00										
Description	BACTERIOCIN PLANTARICI	FACTOR INDUCED GENE 2.		YOP PROTEINS TRANSLOCA	QUINOL OXIDASE POLYPEP	HYPOTHETICAL 14.2 KD P	INTIMIN (OUTER MEMBRAN	HYPOTHETICAL PROTEIN I	POLY [ADP-RIBOSE] POLY	CREATINE KINASE, SARCO	HYPOTHETICAL TRANSCRIP	MAJOR CAPSID PROTEIN (HYPOTHETICAL 12.0 KD P	GLUTATHIONE S-TRANSFER	HEAT SHOCK FACTOR PROT	HEMAGGLUTININ-NEURAMIN	GENE 31 PROTEIN (GP31)						
SOFFICES	PLNA_LACPL	FIG2_YEAST	IDUA_CANFA	YSCA_YEREN	QOX1_BACSU	YOO7_MYCLE	EAEA_HAFAL	YHS3_SACKL	PPOL_SARPE	KCRS_CHICK	YBBB_BACSU	VCAP_HSVEB	YMI4_YEAST	GTA1_RAT	HSF8_LYCPE	HEMA_PI3HW	HEMA_PI3HA	HEMA_PI3HU	HEMA_PI3H4	HEMA_PI3HV	HEMA_PI3HT	HEMA_PI3HX	VG31_BPMD2
DB	: -	П	-	-	Н.	-	Н.	Н	Н	Н	Н	Н	1	H	Н	Н		П	-	-	7	Н	7
Length	48	1609	655	32	649	134	280	341	966	419	529	1376	102	221	527	572	572	572	572	572	572	572	617
% Query Match	100.0	39.5	38.2	32.5	34.7	34.2	33.7	33.7	33.2	32.7	32.2	31.7	31.2	31.2	31.2	31.2	31.2	31.2	31.2	31.2	i.	31.2	31.2
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between the Swiss Institute of Bioinformatics and the EMBL outstation-
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 92397594.
WILSON C., GRISANTI P., FRONTALI L.;
"The complete sequence of a 6146 bp fragment of Saccharomyces cerevistae chromosome III contains two new open reading frames.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
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Pred. No. 1.20e-02;
8; Mismatches 7; Indels
                                                                                                                                                                                                      BACTERIOCIN PLANTARICIN A.
MISSING (IN THE ALPHA CHAIN).
A6083DE9 CRC32;
                                                                                                                                                                                                                                                                        Length 48;
                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S19504; S19504.
PIR; S25345; S23345.
SGD: S125: FIGE
SEQUENCE 1609 AA: 166049 MW; DE974CE8 CRC32;
                                                                                                                                                                                                                                                                        Score 199; DB 1; I
Pred. No. 5.90e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-WAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
FACTOR INDUCED GENE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YEAST 8:569-575(1992).
-!- FUNCTION: REQUIRED FOR EFFICIENT MATING.
-!- INDUCTION: BY MATING PHEROMONES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         655 AA.
                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1609 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FIG2 OR YCR089W OR YCR89W OR YCR1102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                         23 KSSAYSLQMGATAIKQVKKLFKKWGW 48
                                                                                                                                                                                                                                                                                                                                                         1 KSSAYSLQMGATAIKQVKKLFKKWGW 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SACCHAROMYCETACEAE; SACCHAROMYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1092 PSQYSLSTATTTINGIKTVYTTW 1114
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IDUA_CANFA STANDARD; F
Q01634;
01-FEB-1994 (REL. 28, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1992 (REL. 22, CREATED)
                                                                                                                                                                                                                       26
5458 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39.2%;
Local Similarity 34.8%;
hes 8; Conservative
                                                                                                                                                                                                                                                               Local Similarity 100.0%;
les 26; Consermation
                                                                                                                     EMBL; X75323; G452406; -. EMBL; X94434; E217591; -. PIR; A45913; A45913. ANTIBIOTIC; BACTERIOCIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X59720; E264634; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                         48 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       FIG2_YEAST
P25653;
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                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                          Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mucopolysaccharidosis I.";
GENOMICS 14:763-768(1992).
-!- CATALYTIC ACTIVITY: HYDROLYSIS OF ALPHA-L-IDURONOSIDIC LINKAGES IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MENON K.P., TIEU P.T., NEUFELD B.F.; "Architecture of the canine IDUA gene and mutation underlying canine mucopolysaccharidosis I.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DESULFATED DERMATAN.
--- SUBUNIT: MONOMER (PROBABLE).
--- SUBUNIT: MONOMER (PROBABLE).
--- TISSUE SPECIFICITY: FOUND UBIQUITOUSLY.
--- TIM: A SMALLER 63 KDA PROTEIN PROBABLY ARISES FROM IDUA PROTEIN
BY PROTEOLYTIC CLEAVAGE.
--- DISEASE: DEFECTS IN IDUA ARE THE CAUSE OF MUCOPOLYSACCHARIDOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                           STOLIZEUS L.J., SOSA-PINEDA B., MOSKOWITZ S.M., MENON K.P., DLOTT 1 HOOPER L., TEPLOW D.B., SHULL R.M., NEUFELD E.F.; Clolning and characterization of cDNA encoding canine alpha-L-iduronidase. mRNA deficiency in mucopolysaccharidosis I dog."; J. BIOL. CHEM. 267:6570-6575(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                           CANIS FAMILIARIS (DOG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
CARNIVORA; FISSIPEDIA; CANIDAE; CANIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE I (MPS I).
-!- SIMILARITY: BELONGS TO FAMILY 39 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 76; DB 1; Length 655;
Pred. No. 2.93e-02;
8; Mismatches 8; Indels
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7358E9D7 CRC32;
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
ALPHA-L-IDURONIDASE PRECURSOR (EC 3.2.1.76).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A42420; A42420
PROSITE; PSO1027; GIXCOSYL_HYDROL_F39; 1.
PFAM; PF01229; GIXCOSYL_HYDR19; 1.
HYDROLASE; GIXCOSIDASE; LYSOSOME; SIGNAL.
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
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POTENTIAL.
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EMBL; L01059; -; NOT_ANNOTATED_CDS.

EMBL; L01060; -; NOT_ANNOTATED_CDS.

EMBL; L01061; -; NOT_ANNOTATED_CDS.

EMBL; L01065; G552348; -.

EMBL; M81893; G163964; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267 SSIYILEQEQATVQQIRRLFPKFA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-TESTIS, AND FIBROBLAST;
MEDLINE; 93052413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72939 MW;
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              414 4
655 AA;
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MEDLINE; 92202199.
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      SOURCE STREET ST
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                                                                                                                                        SEQUENCE FROM N.A.

STRAIN4439-80 / SEROTYPE 0:9;

MEDLINE; 91317716.

MICHIELS T., VANOOTEGHEM J.-C., DE ROUVROIT C., CHINA B., GUSTIN A.,

BOUDRY P., CORNELIS G.R.;

"Analysis of virc, an operon involved in the secretion of Yop

proteins by Yersinia enterocolitica.";

BACTERIOL. 173:4994-5009(1991).

-1- INDUCTION: AT 37 DEGREES CELSIUS IN THE ABSENCE OF CALCIUM.

-1- BELONGS TO AN OPERON INVOLVED IN THE TRANSLOCATION OF YOP PROTEINS

FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular cloning, sequencing, and physiological characterization of
the gox operon from Bacillus subtilis encoding the aa3-600 quinol
oxidase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
15-UL-1998 (REL. 36, LAST ANNOTATION UPDATE)
415-UL-1998 (REL. 36, LAST ANNOTATION UPDATE)
4201NOL OXIDASE POLYPETIDE I (EC 1.9.3. -) (QUINOL OXIDASE AA3-600, SUBUNIT QOXB) (OXIDASE AA(3) SUBUNIT 1)
                                                                                                         BACTERIA: PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
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BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SANTANA M., KUNST F., HULLO M.F., RAPOPORT G., DANCHIN A.,
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 70; DB 1; Length 32;
Pred. No. 3.91e-01;
6; Mismatches 5; Indels
                                 01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-EBB-1995 (REL. 31, LAST ANNOTATION UPDATE)
YOP PROTEINS TRANSLOCATION PROTEIN A.
                                                                                                                                                                                                                                                                                                                                                                                                       32 AA; 3815 MW; 41DF6051 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      649 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BIOL. CHEM. 267:10225-10231(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                            35.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                      arity 31.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                     EMBL; M74011; G155550; -. PIR; A40361; A40361. PLASMID; VIRULENCE.
              STANDARD;
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                                                                                      ERSINIA ENTEROCOLITICA.
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9 MGATAIKQVKKLFKKW 24
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            YSCA_YEREN
Q01242;
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P34956;
                                                                                                PLASMID PYV
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           A GLASER P., KUNST F., ARNAUD M., COUDART M.P., GONZALES W.,
A GLASER P., KUNST F., ARNAUD M., LUBOCHINSKY B., MARCELINO L., MOSZER I.,
PRESEANE E., SANTANA M., SCHNEIDER E., SCHWEIZER J., VERTES A.,
RAPOPORT G., DANCHIN A.,
"Bacillus subtilis genome project: cloning and sequencing of the 97
Kb region from 325 degrees to 333 degrees.";
L MOL. MICROBIOL. 10:371-384(1993).

-!- FUNCTION: CATALYZES QUINOL OXIDATION WITH THE CONCOMITANT
CONVERSION DURING VEGETATIVE GROWTH.
CONVERSION DURING VEGETATIVE GROWTH.
C -!- COFACTOR: HEMSE A. A3, AND COPPER B.
-!- PATHGARY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
C -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
C -!- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P98002; 1ARI.
OXIDOREDUCTASE; HEME; COPPER; TRANSMEMBRANE; RESPIRATORY CHAIN;
HYDROGEN ION TRANSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COPPER B (PROBABLE).
COPPER B (PROBABLE).
COPPER B (PROBABLE).
COPPER B (PROBABLE).
IRON (HEME A3) (PROBABLE).
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EMBL; X73124; G413962; -.
EMBL; Z99123; E1186315; -.
PIR; B38129; B38129.
PIR; S39693; S39693.
SUBTILIST; BG10584; QOXB.
PROSITE; PS00077; COXI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00115; COX1; 1.
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FRANKEL G., CANDY D.C.A., EVEREST P., DOUGAN G.;
FRANKEL G., CANDY D.C.A., EVEREST P., DOUGAN G.;
"Characterization of the C-terminal domains of intimin-like proteins of enteropathogenic and enterohemorrhagic Escherichia coli, citrobacter freundii, and Haffnia alvel.";

INFECT. IMMUN. 62:1835-1842(1994).

INFECT. IMMUN. 62:1835-1842(1994).
                                                                                                                                                                                                                                           MYCOBĀCTĒRIUM LEPRAĒ.
BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAĒ;
ACTINOMYCETALĒS; CORYNĒBACTĒRINĒAĒ; MYCOBĀCTĒRIĀCĒAĒ; MYCOBĀCTĒRIUM.
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST NNOTATION UPDATE)
INTIMIN (OUTER MEMBRANE PROTEIN) (ATTACHING AND EFFACING PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 68; DB 1; Length 134; Pred. No. 8.97e-01; 8; Mismatches 7; Indels
                                  Length 649;
                                                          8; Indels
IRON (HEME A) (PROBABLE). 7C64B76E CRC32;
                                                                                                                                                                                                                                                                                                     ROBISON K., SMITH D.R.;
SUBMITTED (MAR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SIMILARITY: BELONGS TO THE DEDA FAMILY.
                                 Score 69; DB 1; L4
Pred. No. 5.93e-01;
4; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 AA; 14249 MW; 7F5164A5 CRC32;
                                                                                                                                                                                           01-NOV-1997 (REL. 35', LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35', LAST ANNOTATION UPDATE)
HYPOTHETICAL 14.2 KD PROTEIN B1177_C2_172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         280 AA
                                                                                                                                                         PRT; 134 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -! - SUBCELLULAR LOCATION: OUTER SURFACE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQ
           73838 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 YSLOMGATAIKOVKKLFKKWG 25
                                                                                                 6 SLQMGATAIKQVKKLFKKWGW 26
                                                                                   22 SIALSTIAIIFVLTYFKKWKW 42
                                 34.7%;
ilarity 42.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34.2%;
28.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                           STANDARD;
417 4
649 AA;
                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 94222551.
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                     6
YQO7_MYCLE
Q49642;
01-**
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAFNIA ALVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EAEA OR EAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EAEA_HAFAL
P52869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
            SEQUENCE
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                                      Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-CBS 3082;
MEDLINE; 93289813.
WEINSTOCK K.G., STRATHERN J.N.;
"Molecular genetics in Saccharomyces kluyver1: the HIS3 homolog and its use as a selectable marker gene in S. kluyver1 and Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SACCHAROMYCES KLUYVERI (YEAST).
EUKARYOTA, FUNGI; ASCOMYCOTA, HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                      Length 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
-i- SIMILARITY: BELONGS TO THE EAE/INVASIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST SHOUTATION UPDATE)
HYPOTHETICAL PROTEIN IN HIS3 3'REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                   Score 67; DB 1; L
Pred. No. 1.35e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 107 POLY-SER.
341 AA; 37381 MW; 64772A58 CRC32;
                                                                                                                                                                                                                                                                                                                         NON_TER 1 1
SEQUENCE 280 AA; 30146 MW; FBC2C19D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
ID PPOL SARPE STAR....
AC 011208:
DI 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 341 AA.
                                                                                                                                                                                                                                                                                                                                                                                                        33.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; 214125; E1175791; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.28;
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                                                                                                                                                                                                                                                                 EMBL; L29509; G472359; -. OUTER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 209 PSSIKELKDLYDDWG 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 ATAIKQVKKLFKKWG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 SQVKSLRKVFKKW 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YEAST 9:351-361(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : :| ::|:||||
12 TAIKQVKKLFKKW 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S31236; S31236.
HYPOTHETICAL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
ID YHS3_SACKL
AC Q03000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cerevistae.
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15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
    SO THE TENERS OF THE TENERS OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- SIMILARITY: BELONGS TO THE PARP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                         MEDINE: 94170813.

MASUTANI M., NOZAKI T., HITOMI Y., IKEJIMA M., NAGASAKI K.,
DE PRATI A.C., KURATA S., NATORI S., SUGIMURA T., ESUMI H.;
DE CIONING and functional expression of poly(ADP-ribose) polymerase cond from Sarcophaga peregrina.";
EUR. J. BIOCHEM. 220:607-614(1994).
-! FRUTION: POLY(ADP-RIBOSE] POLYMERASE MODIFIES VARIOUS NUCLEAR PROTEINS BY POLY(ADP-RIBOSYL)ATION. THE MODIFICATION IS DEPENDENT ON DNA AND IS INVOLVED IN THE REGULATION OF VARIOUS IMPORTANT CELLULAR PROCESSES SUCH AS DIFFERENTIATION, PROLIFERATION, AND TUMOR TRANSFORMATION AND THE REGULATION OF THE MOLECULAR
                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
POLY [ADP-RIBOSE] POLYMERASE (EC 2.4.2.30) (PARP) (ADPRT) (NAD(+) ADP-RIBOSYLTRANSFERASE) (POLY[ADP-RIBOSE] SYNTHETASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSFERASE; GLYCOSYLTRANSFERASE; NAD; DNA-BINDING; NUCLEAR PROTEIN;
ADP-RIBOSYLATION; ZINC-FINGER; ZINC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTOMODIFICATION DOMAIN.
NAD-BINDING.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
NUCLEAR LOCALIZATION SIGNAL 1ST PART.
NUCLEAR LOCALIZATION SIGNAL 2SUD PART.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; OESTROIDEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C9E71E28 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 66; DB 1; L
Pred. No. 2.02e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D16482; G538248; -.
PROSITE; PS00347; PARP_ZN_FINGER_1; FALSE_NEG.
PROSITE; PS50064; PARP_ZN_FINGER_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1989 (REL. 11, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY
                                                                                                                                                             SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE; 94170813.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    552 KNSFYKLQLLESDMKNRFWVFRSWGR 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KSSAYSLQMGATAIKQVKKLFKKWGW 26
                                                             SARCOPHAGA PEREGRINA (FLESH FLY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113018 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.2%;
34.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF00533; BRCT; 1.
PFAM; PF00644; PARP; 1.
PFAM; PF00645; zf-PARP; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Conservative
                                                                                                     PTERYGOTA; DIPTERA; BRACH)
SARCOPHAGIDAE; SARCOPHAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    508
19
126
211
232
878
996 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KCRS_CHICK
P11009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA_BIND
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ZN_FING
ZN_FING
DOMAIN
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g
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TRANSFERASE; KINASE; MULTIGENE FAMILY; MITOCHONDRION; TRANSIT PEPTIDE;
                                                                                                                                                                                                                                                                                                                                                                                       MEDINE: 88162838.

HOSSLE J.P., SCHLEGEL J., WEGMANN G., WYSS M., BOEHLEN P.,
EPPENBERGER H.M., WALLIMANN T., PERRIARD J.-C.;

"Distinct tissue specific mitochondrial creatine kinases from chicken brain and striated muscle with a conserved CK framework.";
                                                                                                                                                                                                                                MUCHLEBACH S.M., WIRZ T., BRAENDLE U., PERRIARD J.-C.;
"Evolution of the creative kinases. The chicken acidic type
mitochondrial creatine kinase gene as the first nonmammalian gene.";
J. BIOL. CHEM. 271:11920-11929(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
CREATINE KINASE, SARCOMERIC MITOCHONDRIAL PRECURSOR (EC 2.7.3.2) (S-
MICK) (MIB-CK) (BASIC-TYPE MITOCHONDRIAL CREATINE KINASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                           EUKARYOTA; METAZOA; CHOKDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 65; DB 1; Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CREATINE KINASE, SARCOMERIC MITOCHONDRIAL.
                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 21-419 FROM N.A., AND SEQUENCE OF 40-69 TISSUE-SKELETAL MUSCLE, AND HEART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BIOCHEM. BIOPHYS. RES. COMMUN. 151:408-416(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 3.02e+00;
6; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
DEEOD27E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MITOCHONDRION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS00112; GUANIDO_KINASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M18866; G211526; ALT_FRAME.
PIR; A27708; A27708.
PDB; ICRK; Q7-JUL-97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47084 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.9%;
                                                                                                                                                              SEQUENCE OF 1-39 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                     GALLUS GALLUS (CHICKEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           290 GLKEVERLIKERGW 303
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419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 AIKQVKKLFKKWGW 26
                                                                                                                                                                                    STRAIN=WHITE LEGHORN;
MEDLINE; 96216114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       317 3
419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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SEQUENCE
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RESULT
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                               01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN FEDA-SIGW INTERGENIC REGION
                                                                                                                                                                                          QUIRK P.G., GUFFANTI A.A., CLEJAN S., CHENG J., KRULMICH T.A.; "Isolation of Tn917 insertional mutants of Bacillus subtilis that are resistant to the protonophore carbonyl cyanide
                                                                                                                                                                                                                                                                             STRAIN-168;
LIU H., HAGA K., YASUMOTO K., OHASHI Y., YOSHIKAWA H., TAKAHASHI H.;
SUBMITTED (APR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SIMILARIIY: BELONGS TO THE ARAC/XYLS FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                   BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
PSOSITE; PS01124; HTH_ARAC_FAMILY_2; 1.
PFAM: PF00165; HTH_2; 1.
HYPOTHETICAL PROTEIN; TRANSCRIPTION REGULATION; DNA-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201 H-T-H MOTIF (BY SIMILARITY).
60763 MW; 4CD7344C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 64; DB 1; Length 529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 92295566.
TELFORD E.A.R., WATSON M.S., MCBRIDE K., DAVISON A.J.;
"The DNA sequence of equine herpesvirus-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSDNA VIRUSES, NO RNA STAGE; HERPESVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-1992 (REL. 24, CREATED)
01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)
MAJOR CAPSID PROTEIN (MCP) (CAPSID PROTEIN VP5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 4.48e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
           529 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1376 AA.
                                                                                                                                                                                                                             m-chlorophenylhydrazone.";
BIOCHIM. BIOPHYS. ACTA 1186:27-34(1994).
            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALPHAHERPESVIRINAE; VARICELLOVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB002150; D1020256; -. EMBL; Z99104; E1182097; -. SUBTILIST; BG10834; YBBB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 QMAGISAKHYSESFKKW 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 OMGATAIKQVKKLFKKW 24
                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L19954; G438457; -.
           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201
                                                                                                                                                                 MEDLINE; 94281248.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         529 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                        SACILLUS SUBTILIS.
                                                                                                                                                                                                                                                                                                                          REGULATORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VCAP_HSVEB
P28920;
        KBBB_BACSU
                                                                                                                                  BACILLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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RESULT
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01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
HYPOTHETICAL 12.0 KD PROTEIN IN TUBI-CPR3 INTERGENIC REGION PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTAL_RAT STANDARD; PRT; 221 AA.
P00502;
21-JUL-1986 (REL. 01, CREATED)
01-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
GLUTATHIONE S-TRANSFERASE YA (EC 2.5.1.18) (LIGANDIN) (CHAIN 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ï
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-1- FUNCTION: MAJOR PROTEIN OF THE ICOSAHEDRAL CAPSID.
-1- SIMILARITY: TO OTHER HERPESVIRUSES MAJOR CAPSID PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL PROTEIN YML084W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 31.2%; Score 62; DB 1; Length 102; Local Similarity 42.9%; Pred. No. 9.73e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENTLES S., BOWMAN S., BARRELL B.G., RAJANDREAM M.A.; SUBMITTED (NOV-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                  1376 AA; 152182 MW; E6F464C0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 63; DB 1; L. Pred. No. 6.62e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 AA; 12030 MW; 94F162C2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Mismatches
                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               487 GAYVILPPAGILLDQMRRFFERW 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 SAY-SLOMGATAIKQVKKLFKKW 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 RSSYYSLTINGSTISLLKKYF 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; 246660; G575719; -. HYPOTHETICAL PROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KSSAYSLQMGATAIKQVKKLF 21
                                                                                                                                                                                                                                                                                                                                          EMBL; M86664; G330835; -. PIR; H36799; VCBED6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-S288C / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                COAT PROTEIN
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Q04521;
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                          1 JULOL. CHEM. 257:523-530(1982).

1 J. BIOL. CHEM. 257:523-530(1982).

1 J. BIOL. CHEM. 257:523-530(1982).

1 J. BIOL. CHEM. 257:523-530(1982).

2 - 1 - FUNCTION: CONJUGATION OF REDUCED GLUTATHIONE TO A WIDE NUMBER CONTROL OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A CLOSELY RELATED MULTIGENE FAMILY.
IN ADDITION TO ITS ENZYMATIC ACTIVITY, THE HOMODIMER OF YA CHAINS,
CALLED LIGANDIN, BINDS VARIOUS ORGANIC ANIONS, XENOBIOTICS, AND
AZOCARCINOGEN DYES. IT ISA CYTOSOLIC PROTEIN FOUND IN MANY
MAMMALIAN TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                      KALINYAK J.E., TAYLOR J.M.; "Rat glutathione S-transferase. Cloning of double-stranded cDNA and induction of its mRNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
HEAT SHOCK FACTOR PROTEIN HSF8 (HEAT SHOCK TRANSCRIPTION FACTOR 8)
(HSTF 8) (HEAT STRESS TRANSCRIPTION FACTOR).
                                                                                                                                                   LAI H.-C.J., LI N.-Q., WEISS M.J., REDDY C.C., TU C.-P.D.;
The nucleotides sequence of a rat liver glutathione S-transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
(CLASS-ALPHA) (CLONES PGST94 & PGTR261).
RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. ALPHA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 62; DB 1; Length 221;
Pred. No. 9.73e+00;
3; Mismatches 6; Indels
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; C115D4C3 CRC32;
                                                                 RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                  subunit cDNA clone.";
J. BIOL. CHEM. 259:5536-5542(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00043; gluts; 1.
HSSP; P08263; 1GSF.
TRANSFERASE; MULTIGENE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             221 AA; 25480 MW;
                                                                                                                                                                                                                                                             SEQUENCE OF 45-196 FROM N.A. MEDLINE; 82075944.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 43.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              205 LPMDAKQIEEARKIFK 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; K01931; G204495; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 LOMGATAIKOVKKLFK 22
                                                                                                            SEQUENCE FROM N.A. MEDLINE; 84185691.
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P41153;
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                                                                                                                                                                                                      SCHARE K.D., ROSE S., THIERFELDER J., NOVER L.;
"TWO CDRAS for tomato heat stress transcription factors.";
PLANT PHYSIOL, 102:1355-1356(1993).
-!- FUNCTION: DNA-BINDING PROTEIN THAT SPECIFICALLY BINDS HEAT SHOCK
PROMOTER ELEMENTS (HSE) AND ACTIVATES TRANSCRIPTION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                  EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
ASTERIDAE; SOLANANAE; SOLANALES; SOLANACEAE; SOLANUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSCRIPTION REGULATION; NUCLEAR PROTEIN; DNA-BINDING; ACTIVATOR;
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Pred. No. 9.73e+00;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                          -1- SUBUNIT: HOMOTRIMER.
-1- SUBCELLULAR LOCATION: NUCLEAR.
-1- PIM: EXHIBITS TEMPERATURE-DEPENDENT PHOSPHORYLATION
-1- PIM: SALIBITS!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34DE58C9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHOSPHORYLATION; HEAT SHOCK; MULTIGENE FAMILY.
DNA_BIND 39 133 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -! - SIMILARITY: BELONGS TO THE HSF FAMILY.
LYCOPERSICON PERUVIANUM (PERUVIAN TOMATO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
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POLY-GLN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; S25481; S25481.
PROSITE: PS00434; HSF_DOMAIN; 1.
PFAM; PF00447; HSF_DNA-bind; 1.
HSSP; P22121; 3HSF_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139 143 PO
195 198 PO
527 AA; 57519 MW;
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143
198
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SEQUENCE FROM N.A.
MEDLINE; 94105354.
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protein - protein database search, using Smith-Waterman algorithm Wed Sep 15 10:39:22 1999; MasPar time 5.79 Seconds 245.104 Million cell updates/sec Run on:

Tabular output not generated.

1 KSSAYSLQMGATAIKQVKKLFKKWGW 26 SUS-09-068-507A-1 (1-26) from US09068507A.pep Description: Perfect Score: Sequence:

PAM 150 Scoring table: 179066 seqs, 54579741 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

sptremp19 Database:

1:sp_archea 2:sp_bacteria 3:sp_fung1 4:sp_human 5:sp_invertebrate 6:sp_mamma1 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

SUMMARIES

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 30.932; Variance 45.599; scale 0.678

Statistics:

4.80e+00 4.80e+00 4.80e+00 1.48e+00 2.20e+00 2.20e+00 2.20e+00 3.26e+00 3.26e+00 3.26e+00 3.26e+00 5.45e-02 1.27e-01 1.27e-01 1.27e-01 2.92e-01 1.40e-01 1.48e+00 Pred. No. HYPOTHETICAL 23.1 KD P PHAGE SPP1 DNA SEQUENC PROTEIN TYROSINE KINAS VIRION PROTEIN (FRAGME 457AA LONG HYPOTHETICA NUCLEOSIDE TRIPHOSPHAT PROBABLE MEMBRANE SPAN MYELIN TRANSCRIPTION F PUTATIVE DISEASE RESIS 157AA LONG HYPOTHETICA 650AA LONG HYPOTHETICA GABA-BRIB RECEPTOR. GABA-BRIA RECEPTOR. GLYCOPROTEIN GP14. COSMID C06A8 C-SRC KINASE CEREBRIN-50 Description 015150 061442 P96606 019712 073786 008620 Q66678 017690 049635 038150 037319 054923 844 11 960 11 960 11 218 5 450 13 1170 10 157 1 256 9 256 9 256 9 457 14 Query Match Length DB Score Result

MEDLINE; 98344137

STRAIN-OT3

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ALIGNMENTS

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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARCHAEA; EURYARCHAEOTA; THERMOCOCCALES; THERMOCOCCACEAE; PYROCOCCUS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 822;
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Local Similarity 33.3%; Pred. No. 5.45e-02;
Los 7; Conservative 7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                      TEGUE-BRAIN;
MEDLINE; 98070770.
MEDLINE; 98070770.
KEE Y., YOO J.S., HAZUKA C.D., PETERSON K.E., HSU S.C., SCHELLER R.H.;
SCHELLER R.H.;
"Subunit structure of the mammalian exocyst complex.";
"Subunit structure of SCI. U.S.A. 94:14438-14443(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JOST (TREMBLREL. 07, LAST SEQUENCE UPDATE) 01-JOST (TREMBLREL. 09, LAST ANNOTATION UPDATE) 650AA LONG HYPOTHETICAL PROTEIN.
                                                                               LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                PROC. NATL. ACAD. SCI. U.S.A. 94:14438-14443(1)
EMBL; AF032668; G2827162; -.
SEQUENCE 822 AA; 95105 MW; 38EFF544 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      650 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                               01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQI
01-NOV-1998 (TREMBLREL. 08, LAST ANN
                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    731 TLQLAFIDLRQLLDLFMVWDW 751
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                     PRELIMINARY;
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KAWARABAYASI Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y.,
YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOYAMA A., NAGAI Y.,
SAKAI M., OGURA K., OTUKA R., NAKAZAWA H., TAKAMIYA M., OHFUKU Y.,
FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI A.,
AOKI K., NAKAMURA Y., ROBB T.F., HORIKOSHI K., MASUCHI Y., SHIZUYA H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHÓRDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
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STRAIN-TIF (RAI F(SPF)); TISSUE-CORTEX, AND CEREBELLUM;
MEDLINE; 9722131.
KAUPMANN K., HEGGEL K., HEID J., FLOR P.J., BISCHOFF S., MICKEL S.J.,
MCMASTER G., ANGST C., BITTIGER H., FROESTL W., BETTLER B.;
"Expression clouding of GABA(B) receptors uncovers similarity to
netabolropic glutamate receptors.";
metabolropic glutamate receptors.";
EMBL; Y10370; E311196; -..
PFAM; PF01094; ANF_receptor; 1.
SEQUENCE 844 AA; 95037 MW; 6611F68D CRC32;
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STRAINTIF(FRAI F (SPF)); TISSUE-CORTEX, AND CEREBELLUM;
MEDLINE; 9722131.
KAUPMANN K., HEGGEL K., HEID J., FLOR P. J., BISCHOFF S., MICKEL S.J.,
MOMASTER G., ANGST C., BITTIGER H., FROESTL W., BETTLER B.;
MEXPLESSION CLONING Of GABA(B) receptors uncovers similarity to
metabotropic glutamate receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                "Complete Sequence and Gene Organization of the Genome of a Hyper-thermophilic Archaebacterium, Pyrococcus horikoshii OT3."; DNA RES. 5:55-76(1998).
EMBL; AP000006; D1031515; -. SEQUENCE 650 AA; 75553 MW; EDC92EIE CRC32;
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                                                                                                                                                                                                     37.7%; Score 75; DB 1; Length 650; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 37.7%; Score 75; DB 11; Length 844; Best Local Similarity 87.5%; Pred. No. 1.27e-01; Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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01-NOV-1998 (TREMBLREL. 08,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RATTUS NORVEGICUS (RAT).
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Best Local Similarity
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RA MILSON N. A. AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., TAINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., COLLSON R., AINSCOUGH R., AINSCOUGH R., AINSCOUGH R., AUGUSTON M., DEAR S., JU Z., DUNEIL M., COPPER T., COULSON A., FULTON L., ACATON M., DEAR S., JU Z., DUNEIN R., FAVELLO A., FULTON L., JOHNSTON E., FARTONE M., KERSHAW J., KIRSTEN J., LAISTER M., LATREILLE P., ALGHTNING J., LLOYD C., MCMNERAY A., MORTINGNE B., O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R., SMALDON N., SMITH A., SONHAMMER E., STADER R., SULGTON J., MALLON S., MATSON A., WALTSTON J., WALGHAN K., WATERSTON R., TELLON J., WALLON D., STATH A., SONHAMMER E., STADER R., WALSON J., MATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P., FT. T. Z. M. O'C CONTIGUOUS NUCLEOCITIES SEQUENCE from chromosome III of C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>ب</u>
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HABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
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                                                                                                    Match 37.7%; Score 75; DB 11; Length 960; Local Similarity 87.5%; Pred. No. 1.276-01; es 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36.7%; Score 73; DB 14; Length 950;
47.6%; Pred. No. 2.92e-01;
varive 4: Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NECHBAUER A., BRAUN B., KAADEN O.R., OSTERRIEDER K.; SUBMITTED (JAN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL: X95377; E220695; -. PPAM; PF00606; Glycoprotein_B; 1. SEQUENCE 950 AA: 106568 WW; B2DE30B2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                      EQUINE HERPESVIRUS TYPE 1 (EHV-1),
VIRUSES; DSDNA VIRUSES, NO RNA STACE; HERPESVIRIDAE;
ALPHAHERPESVIRINAE; VARICELLOVIRUS.
                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                 EMBL; Y10369; E311192; 'PFAM; PF00084; Sushi, 2.
PFAM; PF01094; ANF_receptor; 1.
SEQUENCE 960 AA; 108203 MW; CD3A2D9E CRC32;
                                                                                                                                                                                                                                                                                  950 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218 AA.
                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           926 MSMVSALEKQEKKAIKKNWGW 946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NATURE 386:239-246(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 47.68;
                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAENORHABDITIS ELEGANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NATÜRE 368:32-38(1994).
                                                                                                                                                                      298 KLFEKWGW 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                      19 KLFKKWGW 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COSMID CO6A8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-RACH;
                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                         966678;
                                                                                                                                                                                                                                                        LT 5
Q66678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T. 6
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                                                                                                                                         Matches
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                                                                                                                                                                                                                                                        RESULT
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16 QVKKLFKKWGW 26

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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                    STRAIN-OT3;
MEDLINE; 98344137.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T 10
Q49635
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                                                            CT 9
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BUKARYOTA: VIRIDIPLANTAE: STREFTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA;
BUPHYLLOPHYTES; SPERNATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE: ARABIDOPSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XENOPUS LAEVIS (AFRICAN CLAWED FROG). XENOPUS LAEVIS (AFRICALA); ANURA;
EUKARYOTA; METAZOA: CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
MESOBATRACHIA: PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CY. COLUMBIA:
STRAIN-CY. COLUMBIA:
ROUNSLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRANDON R.C.,
SYKES S.M., KAUL S., MASON T.M., KERLAVAGE A.R., ADAMS M.D.,
SOMERVILLE C.R., VENTER J.C.;
SOMERVILLE C.R., VENTER J.C.;
SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; ACOUST312;
EMBL; ACOUST312;
SEQUENCE 1170 AA; 133397 MW; 9B32952B CRC32;
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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34.7%; Score 69; DB 13; Length 450;
Best Local Similarity 41.7%; Pred. No. 1.48e+00;
Best Local Similarity 41.7%; Pred. No. 1.48e+00;
Matches 10; Conservative 5; Mismatches 9; Indels
                                                                                                                                                                                                                             Query Match 36.2%; Score 72; DB 5; Length 218; Best Local Similarity 60.0%; Pred. No. 4.40e-01; Authors 9; Conservative 4; Mismatches 2; Indels Matches 9; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MURPHY S.M., MORGAN D.O.; MURPHY S.M., MORGAN D.O.; MURPHY S.M., MORGAN D.O.; EMBL/GENBANK/DDBJ DATA BANKS. EMBL: #5105430; 62967840; -. SEQUENCE 450 AA; 50807 MW; E9717367 CRC32; SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
PUTATIVE DISEASE RESISTANCE PROTEIN.
                                                                                                                                    SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL; U3849; G1055042; -- W; 1ACF80C3 CRC32; SEQUENCE 218 AA; 25556 WW; 1ACF80C3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
                                    SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1170 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      450 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                               106 IAATSVKQVEKLFOK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                            SEQUENCE FROM N.A.
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                                    LEIMBACH D.;
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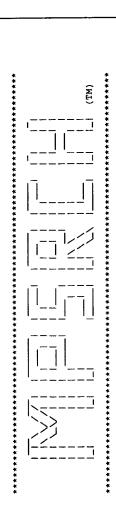
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"Use of an ordered cosmid library to deduce the genomic organization of Mycobacterium leprae.";
                                                                                                                                                                                                                                                                                                                        KAWARNBAYSI Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y.,
YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOYAWA A., NAGAI Y.,
SAKAI M., OGURA K., OTUKA R., NKKAZAWA H., TAKAMIYA M., OHPUKU Y.,
FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI M.,
AOKI K., NAKAMURA Y., ROBB T.F., HORIKOSHI K., MASUCHI Y., SHIZUYA H.,
KIKUCHI H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE; MYCOBACTERIUM. ACTINOMYCETALES; CORYNEBACTERINEAE; MYCOBACTERIACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                          ARCHAEA; EURYARCHAEOTA; THERMOCOCCALES; THERMOCOCCACEAE; PYROCOCCUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete Sequence and Gene Organization of the Genome of a
Hyper-thermophilic Archaebacterium, Pyrococcus horikoshii OT3.";
BNA RES. 5:55-76(1989).
EMBL; AP000005; D1031220; -.
SEQUENCE 157 AA; 18430 MW; 3A304921 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 34.2%; Score 68; DB 1; Length 157; Local Similarity 30.0%; Pred. No. 2.20e+00; Local Similarity 7; Mismatches 7; Indels les 6; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ROBISON K., SMITH D.R.;
ROBISON K., SMITH D.R.;
SUBMITTED (MAR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
SUBMITTED (MO101): G466808;
EMBL; 296801; G466808;
HYPOTHETICAL PROTEIN; TRANSMEMBRANE; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEĞUENCE FROM N.A.
PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
SUBMITTED (JUN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
OLIVER K., HARRIS D.;
SUBMITTED (JUN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                           01-AG-1998 (TREMBLREL. 07, CREATED)
01-AG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
157AA LONG HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 AA; 23114 MW; F162EC6B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 214 AA.
PRT; 157 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL 23.1 KD PROTEIN. MICLS81.27 OR B1177_C1_140. MYCOBACTERIUM LEPRAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 SLEIENKLTREERELYKKWS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 SLOMGATAIKOVKKLFKKWG 25
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              PRELIMINARY;
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                                          Gaps
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
PHAGE SPPI DNA SEQUENCE CODING FOR PRODUCTS REQUIRED FOR REPLICATION
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
PEDLINE: 94172631.
PEDRE X., WEISE F., CHAI S., LUEDER G., ALONSO J.C.;
"Analysis of cis and trans acting elements required for the initiation of DNA replication in the Bacillus subtilis bacteriophage
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
ALONSO J.C., LUDER G., STIEGE A.C., CHAI S., WEISE F., TRAUTNER T.A.;
SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                         BACTERIOPHAGE SPP1.
VIRUSES; DSDNA VIRUSES, NO RNA STAGE; TAILED PHAGES; SIPHOVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MERADLI A.W., KIRSCHNER M.W.;
"Molecular cloning of tyrosine kinases in the early Xenopus embryo:
ldentification of Eck-related genes expressed in cranial neural crest
DEV. DVN. 203:119-014 (hyld) arch.";
EMBL: 011729, G509579;
TYROSINE-PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUKARYOTA, METAZOA, CHORDATA, VERTEERATA, AMPHIBIA, BATRACHIA; ANURA, MESOBATRACHIA, PIPOIDEA, PIPIDAE, XENOPODINAE, XENOPUS.
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   34.2%; Score 68; DB 2; Length 214; 28.6%; Pred. No. 2.20e+00; vative 8; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match
Local Similarity 38.5%; Score 68; DB 9; Length 256;
les 5; Conservative 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV.1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
PROTEIN-TYROSINE KINASE (G56) (FRAGMENT).
                                                                                                                            256 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          256 AA; 29998 MW; 16837A2C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 AA.
                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                XENOPUS LAEVIS (AFRICAN CLAWED FROG).
                                                                                                                                                                                                                                                                                                                              MOL. BIOL. 236:1324-1340(1994).
                                            91 FPKHFGPGHVALVERLFNRWG 111
                                                            S YSLOMGATAIKQVKKLFKKWG 25
                         6; Conservative
                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 ITSIRELMNRWGW 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 IKQVKKLFKKWGW 26
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Query Match
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Q38150
Q38150;
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                        Matches
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091567
091567;
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YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOYAWA A., NAGAI Y.,
BUNAHASHI M., OGURA K., OTUKA R., NAKAZAWA H., TARAMIYA M., OHEUKU Y.,
AOKI K., NAKAMURA Y., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI A.,
KIKUCHI H.;
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARCHAEA; EURYARCHAEOTA; THERMOCOCCALES; THERMOCOCCACEAE; PYROCOCCUS.
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                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete Sequence and Gene Organization of the Genome of a Hyper-thermophilic Archaebacterium, Pyrococcus horikoshii Orl.", EMB. 5:55-76(1998).
EMBI. APO00002; D1030621; -.
SEQUENCE 457 AA; 52090 MW; CD2283F7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                           / Match 33.7%; Score 67; DB 13; Length 51; Local Similarity 41.7%; Pred. No. 3.26e+00; les 10; Conservative 5; Mismatches 9; Indels
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                                                                                                                                                                                                                                                                                                                                                                            Length 225;
                                                                                                                                                                                                                                                                                                                                                                     Score 67; DB 14; Length 225
Pred. No. 3.26e+00;
3; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 67; DB 1; Length 457;
Pred. No. 3.26e+00;
4; Mismatches 3; Indels
                                                                                                                                                                            01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
VARION PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                       DSDNA VIRUSES, NO RNA STAGE; HERPESVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-50G-1998 (TREMBLREL. 07, CREATED)
01-80G-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
NON_TER 1 1
NON_TER 51 51
SEQUENCE 51 AA: 5577 MW; 84274507 CRC32;
                                                                                                                                                                                                                                                                                                                                      SEQUENCE 225 AA; 25754 MW; E3E43F9B CRC32;
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                                                                                         13 KVSDFGLTKEASAIQDSSKLPVKW 36
                                                                                                        PRT;
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34.8%;
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Local Similarity 41.78;
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LT 15 PRELIMINARY; PRT; 646 AA.
037319
01-3AN-1998 (TREMBLREL. 05, CREATED)
01-3AN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-3AN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
NUCLEOSIDE TRIPHOSPHATASE I (EC 3.6.1.15) (NUCLEOSIDE-TRIPHOSPHATASE)
(NUCLEOSIDE TRIPHOSPHATASE PHOSPHOTADOLASE).
(NUCLEOSIDE TRIPHOSPHATASE PHOSPHOTADOLASE).
(NUCLEOSIDE TRIPHOSPHATASE PHOSPHOTADOLASE).
VIRUSES; DSDNA VIRUSES, NO RNA STAGE; POXVIRIDAE; ENTOMOPOXVIRINAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 33.7%; Score 67; DB 14; Length 646; Best Local Similarity 54.5%; Pred. No. 3.26e+00; Andels 0; Gaps Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM S.A.
SETIMACLONAL ISOLATE WT#2/011293;
STRAIN-CLONAL ISOLATE WT#2/011293;
STRAIN-CLONAL ISOLATE WT#2/011293;
STSKANTHA A., OSBORNE R.J., DALL D.J.;
STRAIN-CLONAL OSBORNE R.J., DALL D.J.;
I. GATALYTIC ACTIVITY: NTP + H(2)0 = NDP + PHOSPHATE.
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| 14 ||KQVKKLFKKW 24
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n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn Wed Sep 15 10:38:16 1999; MasPar time 262.06 Seconds 1205.840 Million cell updates/sec Run on:

Tabular output not generated.

1 ATGATGATATTTAAAAAACT........AAATTTTTACCCATGGTAA 114 TACTACTATAAAATTTTTTGA......TTTAAAAATGGGTAGCAATT >US-09-068-507A-2 (1-114) from US09068507A.seq 114 Description: Perfect Score: N.A. Sequence:

TABLE default Gap 6 Scoring table:

646147 seqs, 1385953633 bases \times 2 Searched:

Dbase 0; Query 0

STD :

Nmatch

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

1:em_bal 2:em_ba2 3:em_fun 4:em_htg 5:em_huml 6:em_hum2
7:em_in 8:em_om 9:em_or 10:em_ov 11:em_pat 12:em_ph
13:em_tpl 14:em_ro 15:em_sts 16:em_v1
genbank111 Database:

17:gb_bal 18:gb_ba2 19:gb_htg1 20:gb_htg2 21:gb_in1 22:gb_in2 23:gb_om 24:gb_ov 25:gb_pat 26:gb_ph 27:gb_pl 28:gb_pl2 29:gb_pr1 30:gb_pr2 31:gb_pr3 32:gb_ro 33:gb_st 34:gb_ets 35:gb_sy 36:gb_un 37:gb_ri

Mean 9.118; Variance 6.864; scale 1.328 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Query Process Pr			dF			CHANGE		
5873 17 AF002276 Lactobacillus sake ind 7 7597 17 LSSAKACNP L.sake spla, sppa, spp 7 10772 21 AF012089 Drosophila melanogaste 3 216021 31 HUAC004787 Homo sapiens Chromosom 7 218 25 166494 Sequence 14 from paten 1056 23 MV087256 Mustela vison GT dinuc 4 1072 21 AF012089 Drosophila melanogaste 4 1072 21 AF012089 Drosophila melanogaste 4 31933 22 CELY50F7A Caenorhabditis elegans 4 4996 21 CER43619 Homo sapiens chromosom 4 4996 21 AC002489 Homo sapiens chromosom 4 4996 21 AC002489 Homo sapiens chromosom 4	Result No.	Score	Query	Length D		Д	Description	Pred. No.
7597 17 LSSAKACNP L.sake spiA, sppA, spp 7 10772 21 AF012089 Drosophila melanogaste 3 216021 31 HUAC004787 Homo sapiens Chromosom 2 216021 31 HUAC004787 Homo sapiens Chromosom 2 7218 25 166494 Sequence 14 from paten 1 1056 23 MV087256 Mustela vison GT dinuc 4 10772 21 AF012089 Drosophila melanogaste 4 31933 22 CELY50F7A Caenorhabditis elegans 4 4 4996 21 CER43F8A Caenorhabditis elegans 4 4 4018 19 AC002489 Homo sapiens chromosom 4 4 1073 21 AC002489 Homo sapiens chromosom 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		114	100.0	5873 1	7	F002276	Lactobacillus sake ind	7.64e-44
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ALIGNMENTS

Lactobacillus sake inducing peptide preprotein (sppIP), histidine protein kinase homolog (sppK), response regulator homolog (sppK), sakacin kinase homolog (sppK), response regulator homolog (sppK), sakacin P preprotein (sppA), putative sakacin P immunity protein (sppA) and putative AIP-dependent translocator protein (sppI) genes, complete cds.	Lactobacillus sake Eubacteria; Firmicutes; Low G+C gram-positive bacteria; Lactobacillaceae; Lactobacillus. 1 (bases 1 to 5873) Eijsink, VG., Brurberg, M.B., Middelhoven, P.H. and Nes, I.F. Induction of bacteriochi production in Lactobacillus sake by a	secreted peptide 1. Bacteriol. 178 (8), 2232-2237 (1996) 96.18690 2 (bases 1 to 5873) 2 usurberg, M.B., Nes, T.F. and Eljsink, V.G. Pheromone-induced production of antimicrobial peptides in Lactobacillus	OL. Midroblol. 26 (2), 347-360 (1997) 98043507 3 (bases 1 to 5873) Brurberg,M.B. and Eijslnk,V.G.H. Submitssion Submitted (05-MAY-1997) Plant Pathology, The Norwegian Crop Research Institute, Ass 1432, Norway	Location/Qualifiers 1.5873 /organism="Lactobacillus sake" /strain="LTH673" /db_xref="taxon:1599"
RESULT 1 LOCUS DEFINITION 1 F F F F F F F F F F F F F F F F F F F	 ORGANISM I REFERENCE I AUTHORS I	REEL	JOURNAL MEDLINE REFERENCE AUTHORS TITLE JOURNAL	FEATURES Source

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LEGTTALGLYKTAENIGFETKAIEADMSLFEVADLPFPFIAHVLKKKRAITILCCTRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lactobacillus sakei
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
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Tichaczek, P.S., Vogel, R.F. and Hammes, W.P.
Cloning and sequencing of sakP encoding sakacin P, the bacteriocin
produced by Lactobacillus sake LTH 673
Microbiology 140 (Pt 2), 361-367 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sakacin P; spiA gene; sppA gene; sppE gene; sppK gene; sppR gene;
                                                                                                                                                                                                                                                                                                                                                                                               /product="putative ATP-dependent translocator protein"
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/db_xref="PID:92735692"
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Huhne,K., Axelsson,L., Holck,A. and Krockel,L.
Analysis of the sakacin P gene cluster from Lactobacillus sake
Lb674 and its expression in sakacin-negative Lb. sake strains
Microbiology 142 (Pt 6), 1437-1448 (1996)
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Purification and cloning of sakacin 674, a bacteriocin from
Lactobacillus sake Lb674
FEMS Microbiol. Lett. 115 (2-3), 143-149 (1994)
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100.0%; Score 114; DB 17; Length 5873;
Best Local Similarity 100.0%; Pred. No. 7.64e-44;
Matches 114; Conservative 0; Mismatches 0; Indels 0,
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248542
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KEYWORDS
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                       Huehne, K.
Huehne, K.
Direct Submission
Submitted (28-FBB-1995) Huehne K., Federal Centre for Meat
Research, Microbiology and Toxicology, E.-C.- Baumann-Strasse 20,
Kulmbach, Bavaria, FRG, D-93326
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'function "putative protein conferring immunity to sakacin
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                                                                          /traislation-"MDKEFLESSEYSARFKNFSTLLIMPIAVLLCLVCIFSFFGKRE
ITIEGGOLTTWKQIFILQASTNSVLKQNYLKEGKFYKKGGTLLYYQNTKNONQRRLL
EKQQDNLSYQITSLETLKASIRSNQDOFENNDOFGYRDLLRGYLDORQYYLIENQWYT
DKAATSTTKQOTIALAIMORTIORDOTNIDAYQALYGSIKTNKYYSSTGKYYVLIENGWYT
TKVKAMSDKNEQSGLKADILATQQQIDSLQGSIANAENGKYVKARKGYKHTYNN
GGIKYTSAGTSMARIYYKAKGSLGYETQTLKQTISDSKRYVKARKGYLHYDHY
GGIKYTSAGTSMARIYYTVLADQKRKKTELIPYDDISSSYKIGQRLAKKITRNYPRPII
IEGKINQISVSPTVINGSSYYIIGLATISNNNRKLLHYGWTGKIAIITGKTTFFNYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF012089 10772 bp DNA INV 05-AUG-1997
Drosophila melanogaster cysteine proteinase-1 (CP1) gene, complete
cds, and phenylalanyl tRNA synthetase gene, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 4546 to 4553)
Gray, Y.H., Tanaka, M.M. and Sved, J.A.
P-element-induced recombination in Drosophila melanogaster: hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J (bases 1 to 10772)
Gray, Y. H. M., Sved, J. A., Preston, C. R. and Engels, W. R.
Gray, Y. H. M., Sved, J. A., Preston, C. R. and Engels, W. R.
Submitted (100-JUN-1997) School of Biological Sciences, University of Sydney, Biology Al2, Sydney University, NSW 2006, Australia
Location, Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster
Eukaryotae, mitochondrial eukaryotes; Metazoa; Arthropoda;
Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gray, Y.H.M., Sved, J.A., Preston, C.R. and Engels, W.R. Structure of the cysteine proteinase (CP1) gene of Drosophila melanogaster and associated mutational effects
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/gene="CP1"
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                                                                                                                                                                                                                                                                                                                       Length 7597;
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Pred. No. 7.64e-44;
0; Mismatches 0; Indels
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/db_xref="taxon:7227"
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                                                            /db_xref="SPTREMBL:Q48873"
/protein_id="CAA88431.1"
/db_xref="PID:g695621"
/db_xref="G1:695621"
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AF012089.1 GI:2305220
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/gene="CP1"
872. .1000
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Best Local Similarity 100.0%;
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HFRKSGVLVSLSEQNLVDCSTKYGNNGCNGGLMDNAFRYIKDNGGIDTEKSYPYEAID
DSCHFNKGTVGATDRGFTDIPQGDEKKMAEAVATVGPVSVAIDASHESFQFYSEGVYN
EPQCDAQNLDHGVLVVGFGTDESGEDYWLVKNSWGTTWGDKGFIKMLRNKENQCGIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MLLTLRVQGARHWLKSTRCLASSAAPAKSPSSPPQLEVSGSTYA
POPRTWATEXTEXTVGARHLGTDHPLSIRQRIVNEFYGATRRORGNELESVDGMN
PVTVQQNFDNLLIPADHVSRQKSDCYINQQHLLRAHTTAHQVELISGGLDNFLVVG
EVYRRDEIDSTHYPVFHQADAVRLVTKOKLFERNFGLELEEFTWSGTLADPKLILDHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSWTKPNSPATRRAVKLMEHEMKHVLVGLTKDLFGPRIKYRWVDTYFPFTQPSWELEI
YFKDNMLEWAVLGGGIMHEILQASGYHQSIGYAFGOGLERLAWYLEDIDIRLFWSNDS
GFELSOFSEKDLHNLEWKYRPTSTYPQCTNDLSFWLPQDIEVDAGFSPNDFYDLYRSVAG
DWVEQISLVDKFKHPKTGKSSVCFRIVYRHMERTLIQAEVNEIHKQIASASVDSFNVO
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Homo sapiens Chromosome 16 BAC clone CIT987SK-A-952F10, complete
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  Join(2328. .2426,6476. .6690,6751. .7462)
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Pred. No. 3.81e-02;
52; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                 /note="insertion site of P(CaSpeR)(50C)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product-"phenylalanyl tRNA synthetase"
/protein_id="ARB5750.1"
/db_xref="PlD:9230522"
/db_xref="GI:2305222"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="phenylalanyl tRNA synthetase"
join(8110. .9300,9370. .>9532)
/note="potential orf"
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                                                                                                                                                                                                                                                                                /gene="CP1"
/546.
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6476. .6690
/gene="CP1"
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/gene="CP1"
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/gene="CP1"
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6751. 7707
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Best Local Similarity 16.7%;
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'number=2
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ORGANISM

REFERENCE AUTHORS JOURNAL REFERENCE AUTHORS TITLE

TITLE

JOURNAL

REFERENCE AUTHORS

JOURNAL

COMMENT

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L SUBMITTER (24-JUL-1998) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA
On Jul 24, 1998 this sequence version replaced gi:3241936.
Address all correspondence to: Mark Adams The Institute for Genomic Research 9712 Medical Center Dr. Rockville, MD 20850, USA e-mail address: humgenétigr.org. The Orienterion of the Sequence is from SP6 end to T7 end. Genes were identified by a combination of five methods including: XGRAIL (available by anonymous ftp from arthur.epm.ornl.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris/GENSCANW.html)searches of the complete sequence against a peptide database, and the human gene index database at TIGR (http://www.tigr.org/tdb/hgi/hdi.html).
Genes without peptide homolgy having spliced EST hits are termed 'Unknown gene product'. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/).
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/note="7608, STS1-cSRL-24g1-uA/cSRL-24g1-u2, Chr. -, Homo
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                         HUAC004787 216021 bp DNA PRI 24-JUL-1998
Homo sapiens Chromosome 16 BAC clone CIT9875K-A-952F10, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-JUN-1998) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA, Email:
                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 216021)

Adams, M.D., Loftus, B.J., Zhou, L., Crosby, M., Fuhrmann, J., Mason, T.M., Brandon, R., Kim, U.J., Kerlavage, A.R. and Venter, J.C. Homo sapiens Chromosome 16 BAC clone CIT987SK-A-952F10
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175801. .175945
17602. .175944 CHLC.GCT10B02, Chr. -, Homo saptens"
/db_xref="dbsTs:G09703"
175810. .175945 CHLC.GCT15C04, Chr. -, Homo saptens"
/db_xref="dbsTs:G09935"
199463. .199572
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/note="7766, SIS1-cSRL-27g3-uA/cSRL-27g3-u2, Chr.
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Pred. No. 2.65e-01;
48; Mismatches 34; Indels 0;
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/note="9824, WI-3555, Chr. 16, Homo sapiens"
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60960 a 51778 c 49172 g 53987 t
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/db_xref="taxon:9606"
/chromosome="16"
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Adams, M.D. and Loftus, B.J.
Direct Submission
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Adams, M.D. and Loftus, B.J.
Direct Submission
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27765. .27872
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AC004787.1 GI:3337381
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Best Local Similarity 15.5%;
Matches 15; Conservative
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RESULT
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Submitted (24-JUL-1998) The Institute for Genomic Research, 9712

Medical Center Dr., Rockville, WD 20850, USA

On Jul 24, 1998 this sequence version replaced gi:3241936.

Address all correspondence version replaced gi:3241936.

Address all correspondence to: Mark Adams The Institute for Genomic Research 9712 Medical Center Dr. Rockville, MD 20850, USA e-mail address: hungen@tigr.org. The orientation of the sequence is from sp6 end to 77 end. Genes were identified by a combination of five methods including: XGRAIL (available by anonymous ftp from arthur.epm.ornl.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris/GENSCANW.html)searches of the complete sequence against a peptide database, and the Human gene Index database at TIGR (http://www.tigr.org/tdb/hgi/hgi.html).

Genes without pepetide homolgy having spliced EST hits are termed 'Unknown gene product', Genes encoding tRNAs are predicted by Location/Qualifiers

I. 216021

I. 216021
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/note="7608, STS1-cSRL-24g1-uA/cSRL-24g1-uZ, Chr. -, Homo
                                                                                                                                                                                                                                                       Direct Submission
Submitted (02-JUN-1998) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA, Email:
bjloftus@tigr.org
             Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 21601);
Adams, M.D., Loftus, B.J., Zhou, L., Crosby, M., Fuhrmann, J., Mason, T.M., Brandon, R., Kim, U.J., Kerlavage, A.R. and Venter, J.C. Unpublished
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175801. 1758045
17010="ld084, CHLC.GCT10B02, Chr. -, Homo sapiens"
/db_xref="dbsTs:G09703"
175810. 175945
17010="16316, CHLC.GCT15C04, Chr. -, Homo sapiens"
/db_xref="dbsTs:G09935"
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/note="7766, STS1-cSRL-27g3-uA/cSRL-27g3-uZ, Chr.
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Pred. No. 2.65e-01;
40; Mismatches 15; Indels 1;
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/note="9824, WI-3555, Chr. 16, Homo sapiens"
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51778 c 49172 g 53987 t
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/db_xref="taxon:9606"
/chromosome="16"
/map="#16921-22"
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Adams, M.D. and Loftus, B.J.
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Matches 10; Conservative
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(a. Dases: 1 to 1056)

Brusgaard, K., Shukri, N.M., Malchenko, S., Koroleva, I. and Lohi, O. Direct Submission

Submitted (27-JNN-1997) Breeding and Genetics, Danish Institute of Animal Science, Blichersalle K25, Tjele 8830, DK

Location/Qualifiers

1. 1056
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1482 YYYCYYYYYYYCMGRAMMAAAWYYKRRSCMAWYYYMRGRARKTYYYMARRRGCARSYKK 1541
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                             97 ITTGTTTAATCTTATGAATAAAATTAGAACTATTTCCTGCCATACCACCGTTTATTTTT 38
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Mustela vison GT dinucleotide repeat, chromosome 1q.
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Pred. No. 1.76e+00;
41; Mismatches 16; Indels
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                                                                                                                                                           PAT
                                                             1542 YMAMYWAAWTTWCAAAAMAAMYTTYYWMMWYYKKWMY 1578
                                                                               37 GCAATTCTTTTCTGAAAGTTTTTTAAATATCATCAT 1
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Sequence 14 from patent US 5670367.
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/db_xref="taxon:9667"
/chromosome="1"
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complement(300. .320)
/standard_name="1167R"
221 c 210 g 2
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1491 c 1486 a
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Best Local Similarity 15.9%;
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Nysoideae; Camptotheca.

1 (bases i to 743).

Maldonado-Mendoza.I.E. Vincent.R.M. and Nessler.C.L.
Molecular characterization of three differentially expressed
members of the Camptotheca acuminata 3-hydroxy-3-methylglutaryl CoA
reductase (HMGR) gene family
Plant Mol. Biol. 34 (5), 781-790 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product-"3-hydroxy-3-methylglutaryl coenzyme A reductase"
/protein_id="AAB69727.1"
/db_xref="PID:g1763234"
/db_xref="GI:1763234"
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LTNGVFFTLFFSVAYFLLHRWREKIRTSTPLHIVTVSELAALISLIASVIXILGFFGI
DFVQSFTTRASHDSWDVEYDNDDRFLLEEDSRGFGCAAAIDRSLVPPOVAAVAPBKPK
VYDEVPVATPTSEEDDER TSSLESTRLGNCKAAAIRREALGRLTGKS
LAGLPLDGFDYESILGOCCEMAVGYVOMAVGIAGPLLLGGREYLVPMATTEGCLVAST
NRGCKAIYASGGATSVILRDGMTRAPVVRFGTAKMSAELKFFLEDPRNFDTLAVVFNK
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STGMCSDRYKRPAVNATEGRGKSVVCPSEI IKEBVVRKVLKTNYASLVBELNMLKNTTGS
AMAGALGGFRAHASHVYTAYTATGODPAQNVESSHCITMMRNVNORKDLHVS
IEVIVGGGTQLASQSACLNLLGVKGASKESPGSNSRLLATIVAGSVLAGELSLMSAIA
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Submitted (21-SEP-1996) Biology, Texas A & M University, College
Station, TX 77843-3258, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tlssue_type="leaf"
join(2075. .3075,4301. .4482,5287. .5638,6302. .6536)
/EC_number="1.1.1.34"
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1 ATGATGATATTTAAAAAACTTTCAGAAAAAGAATTGCAAAAAAATAAACGGTGGTATGGCA 60
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Eukaryothas, Viridiplantae, Charophyta/Embryophyta group;
Embryophyta; vascular plants; seed plants; Magnoliophyta;
Magnoliopsida; Cornanae; Cornales; Cornineae; Cornacees;
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Pred. No. 4.438+00;
....matches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Camptotheca acuminata" /db_xref="taxon:16922"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 TAAAAATTTGTTTAATCTTATGAATAAAATTAGAACTATT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 7430)
Maldonado-Mendoza, I.E. and Nessler, C.L.
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Best Local Similarity 82.5%;
Matches 33; Conservative
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EVYRRDEIDSTHYPVFHQADAVRLVTKDKLFERNPGLEFEFEWSGTLADPKLILPHP
SSWTKANKLMEFHZHQKSGVYGSIGYAFGVGLERLAWVLFPDTDIRLFWSNDS
SFRTDNWLEVLGCGTMRHEILQRSGVYQSIGYAFGVGLERLAWVLFPDTDIRLFWSNDS
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DWTEQISLVDKFKHPRTGKSSVCFRIVYRHMERTLTQAEVNBIHKQIASASVDSFNVQ
-v
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'Milson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M., Bonfield, J., Burton, J., Connell, M., Coppey, T., Cooper, T., Cooper, T., Cooper, T., Cooper, T., Jier, M., Donson, M., Dear, S., Du, Z., Durbin, R., Favello, A., Jones, M., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laighting, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thierry-Miley, J., Thomas, K., Vaudin, M., Walkinson-Sproat, J. and Wohldman, P., Weinstock, L., Walkinson-Sproat, J. and Wohldman, P.
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Submitted (03-FEB-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 26; DB 21; Length 10772;
Pred. No. 4.43e+00;
33; Mismatches 20; Indels 0; Gaps
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                                          /product-"phenylalanyl tRNA synthetase"
join(8110. .3300,9370. .>9532)
/note-"potentlal orf"
/codon_start-1
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Strong,C., Tin-Wollam,A. and Harper,M.
He sequence of C. elegans cosmid Y50F7A
Unpublished (1999)
3. (bases 1 to 31933)
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                    oin(<8110. .9300,9370.
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Caenorhabditis elegans
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Best Local Similarity 19.7%;
Matches 13; Conservative
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/number=4
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EERFRAKIFNENKHKAAKHNORFAEGKVSFKLAVNKYADLLHHEFRQLMNGFNYTLHK
QLRAADESFKKVTFISPAHYTLDKSVDWRTKGAYTAVKDQGHGGSCMAFSSTGALEGG
HFRKSGVLVSLSEDWIDDCSFKYGNORGNGGLMDNAFRYIKDNGGIDTEKSYPYEAID
DSCHFNKGTVGATDRGFTDIPQGDEKKMAEAYATVGPVSVALDASHESFOFYSEGYYN
EPQCDAQNLDHGVLVVGFGTDESGEDYMLVKNSWGTTWGDKGFIKMLRNKENQCGIAS
               Drosophila melanogaster cysteine proteinase-1 (CP1) gene, complete cds, and phenylalanyl tRNA synthetase gene, partial cds.
                                                                                                                                                                                          Drosophila melanogaster

Bukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;

Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 4546 to 4553)

2 (ary X.H., Tanaka,M.M. and Sved,J.A.

P-element-induced recombination in Drosophila melanogaster: hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished

3 (bases 1 to 10772)

Gray, Y.H.M., Sved.J.A., Preston,C.R. and Engels,W.R.

Direct Submission
Submitted (30-JUN-1997) School of Biological Sciences, University Sydney, Biology Al2, Sydney University, NSW 2006, Australia Location,Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gray, Y.H.M., Sved, J.A., Preston, C.R. and Engels, W.R. Structure of the cysteine proteinase (CP1) gene of Drosophila melanogaster and associated mutational effects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
joln(872=1000,2310. .2426,6476. .6690,6751. .7707)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(2328. .2426,6476. .6690,6751. .7462)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="cysteine proteinase-1"
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872. .7707
                                                                                                                                                                                                                                                                                                                                                                                           Genetics 144 (4), 1601-1610 (1996)
          DNA
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4546. .4553
/gene="CP1"
       10772 bp
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872. .1000
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06-FEB-1999

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Department of Genetics, Washington University, St. Louis, MO 63110, USA, and Sanger Centre, Hinxton Hall Cambridge CB10 IRQ, England e-mail: rw@nematode.wustl.edu and jes@sanger.ac.uk
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NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone

NEIGHBORING COSMID INFORMATION:

This is a segment of the YAC Y50F7, sequenced to span the gap between T23F4 and F53A10. The 5' cosmid is T23F4, 200 bp overlap; 3' cosmid is F53A10, 200 bp overlap. Actual start of YAC Y50F7 is at base position 25978 of CELK02E7; actual end is at 12429 of CELF56D12.

NOTES:

Coding sequences below are predicted from computer analysis, using the program Genefinder(P. Green and L. Hillier, ms in preparation).

Location/Qualifiers

1. 31933
/organism="Caenorhabditis elegans"
/strain="Bristol N2"
/strain="Bristol N2"
/strain="Bristol N2"
/clone="Y50F7A"
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gene '750F7A"

CDS /gene="Y50F7A."
CDS /gene="Y50F7A."
/codon start="/codon start="

16223. 30367

/gene="Y50F7A.1"

join(16223. 16359,29919. 30015,30197. 30274,30353. 30367)

/gene="Y50F7A.1"

/gene="Y50F7A.1"

/note="contains weak similarity to human LGN protein
(GB:165499); coded for by C. elegans cDNA CEESH91R"

/codon_start=1

/protein_id="AAD12830.1"

/db_xref="BD:94226118"

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/translation="MDWIYSWKDSIFYGMCSCSGSPSYHEKDVPHPHDRLDMPLQLKA

XRRNELNAEGYYRDLERWHERGLETTGINYNAEKSEDFLNMIERMQSNRLDDQRCEMP

BASE COUNT 10129 a 5407 c 4976 g 11421 t ORIGIN Db 20084 ATTAAAAAATTTTCAAAAAAAATTCCAAAAAAAA 20121

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Gaps

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6; Indels

0; Mismatches

Query Match 22.8%; Best Local Similarity 84.2%; Matches 32; Conservative

Score 26; DB 22; Length 31933; Pred. No. 4.43e+00;

Oy 9 ATTTAAAAACTTTCAGAAAAGAATTGCAAAAAAAA 46

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bin/display/db=wormace&class_Sequence &object=Y43F8A

bin/display/db=wormace&class_Sequence &object=Y43F8A

Current sequence finishing criteria for the C. elegans genome
sequencing consortium are that all bases are either sequenced
unambiguously on both strands, or on a single strand with both a
dye primer and dye terminator reaction, from distinct subclones.

Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is NOT necessarily the entire insert of
coverlapping sections once, or longer because we only sequence
overlapping sections once, or longer because we arrange for a small
overlap between neighbouring submissions.

IMPORTANT: This sequence is not the entire insert of clone Y43F8A.

IMPORTANT: This sequence is not the entire insert of clone Y43F8A.

IMPORTANT: This sequence we only sequence overlapping sections
once, or longer because we arrange for a small overlap between
neighbouring submissions.

The true left end of clone Y43F8 is at 1 in this sequence. The true
left end of clone C25F9 is at 38756 in this sequence. The true
right end of clone C25F9 is at 38756 in this sequence.
                                                                                                                                                                                                                                                                           Caenorhabditis elegans
Sukaryota: Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 38856)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wilson, R., Anscough, R., Anderson, K., Baynes, C., Berks, M., Wilson, R., Anscough, R., Connell, M., Copsey, T., Cooper, J., Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Durbin, R., Favello, A., Johnston, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Laterille, P., Lighthing, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Watson, K., Watson, M., Weinstock, L., Wilkinson-Sproat, J. and Wohldman, P.
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                                                         Caenorhabditis elegans cosmid Y43F8A, complete sequence. AL032640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (29-OCT-1998) Louis, MO 63110, USA. E-mail:
jes@sanger.ac.uk or rw@nematode.wustl.edu
2 (bases 1 to 38856)
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/db_xref="taxon:6239"
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/gene="Y43F8A.1"
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/db_xref="PID:e1350420"
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/qene="Y43F8A.1"
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                                                                                                                                                                  AL032640.1 GI:3810703
                                38856 bp
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                                    CEY43F8A
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11
                                                                 DEFINITION
ACCESSION
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1 5.3

gene

CDS

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/translation="MGVYT1IFLYALTSSVFFPVFQSLIFYRACITLSNSTEPEIACK
SKETTARDNSVHSMSSVILMASSTGLCVSAFFTSRWYGHLSDVKSRKLAFLIPFIGLF
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ARLEGTISLGSTLSLGSTSSOLKNFGTGAFFLVAHFIAFNAVFRRDPEKPDLQEK
CVKRKPFCHGTDLKDKKRPPFSSTNLKTLYFSFACSYFPFIGSTRILFFYLKHFFWGA
EEFGYLKAMNTGMTIMSLALYPFLKNLGITDIRLAIFGLTRSIGRAWYAVAWEGWT
                                                                                                                                                                                 VFIVVFFEMFSKFPATAMRSSIATNVGEHERGLAFSLVAVIEALCNLTSSWVFHLAWP
LSLNVFPQLSFVIMPIIILPAITLMILNMRYLEAPELNPEDLTTSIKKSDDISENNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTG: C3HC4; D1-hydrolfolate reductase; DNA directed RNA polymerase
II; Fibronectin type-III domains; Proteasome A-type subunit; Serine
threonine protein kinase; U4/U6 small nuclear ribonucleoprotein;
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Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoldea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                        37699. .37771
/gene="Y43FBA.L1"
/note="A1G His H-tRNA; predicted using tRNAscan-SE-1.11;
preliminary prediction; similar to tRNA-H1s"
37699. .37771
/gene="Y43FBA.L1"
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Current sequence finishing criteria for the C. elegans genome
sequencing consortium are that all bases are either sequenced
unambiguously on both strands, or on a single strand with both a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           For a graphical representation of this sequence and its analysis
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Caenorhabditis elegans cosmid C36B1, complete sequence.
280215
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6764 g 12407 t
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             /db_xref="GI:4008434"
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Best Local Similarity 86.1%;
Matches 31; Conservative
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24742. .24981,25028. .25159)
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                                                                                                                                          join(25447. .25745,26752. .27030,27678. .28025,28756. .28939)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAA21641.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORRAEKGAEPKILAQVILYPLLQLVDLOMISYRYFHKRLTGIAFVDPASVAFYYMLYA
GIPLEKAKELVPIVLINGHVKPDYREKIDKLLTYRTTIESTHTVNTTKIPKRWEIVEN
SEAQNLLEKVIFDPNFSPIMRENLENLPKSLIVTCEYDVLRDEGLIYSERLAASGVPT
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VFFNILHIFILLINKSMRRQATNVLIIGIAISDIFYLFYYVEGGTREFLENGIPCKCRP
KKTEFLAYYIWIVTIFKDVFFRVSAFSGVSLALIRYLVMKYGARINIRVYYTTSTSWA
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RQISTKFLYIDGVFKIIPPILYPFLAFGLLWELKKARDSRKILMRKGEEHEMVHYTKL
VIFWTIGYFLAETPVGISYFYLAYNMGEDFGIIFLANNITVIFVTFLIINSSIHCFFC
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30712. .30895,31865. .32031,32228. .32390,32663. .32813,
33997. .34109,34216. .34299))
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25447. .28939
/gene="Y43F8A.4"
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                                                                 SYLOPFYNAPTOLFWRRY"
16922. . 20371
                                                                                                                                                                                                                   /gene="Y43F8A.2"
                                                                                                      16922. .203/1
/gene="Y43F8A.2"
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.23294,23337. .23487)
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IVTAGWSGSVAVWKREQCAQEIKFIGHSSQAGCARPHPGAFTONDYSSLNVVSCSYDG
TYLLMSLLSGESPIGELEQHPQRYSKYAFHPWGHTATACFEDSTWRWYDTTTKKELLYO
EGHSKSVADVAFHPDGALTGGHDCYGRWDMRTGRCIMFLDGHTKEIHSYEMPNO
YEMITGSSDNSMKWPDLRMRNNTYTMRAHTSVYTRVRADAAGQYLVSASFDCTLKMWS
TTGWQPLRQLQGHDTRILCVDISPDGQMMCSSAFDRTFKLMAQSDY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MAENGNFAVPAPPRQFGSLANAESVNAILNAQQQNHGPTVSLER
MEVSNQADSRHDAEWFAEFDRRRRRARTLTLPTDDVQVKLKLRALNQPICLFGEDALDR
RERLRALLSTMSEDEIAAVLHTDEVNADKADEETVTWYHRGPIELRMARVSIADFSLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="Mpyangpulevteltndlikfvlwdtdlsvanslrrvfmaevpt
ildnwoldfurtsvlhdeftahrmeltefisprybrkmytyfrdceafefedesipfi
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KGQEINLKAVTKKGFGKEHAKWNPTCGVAFEYDDDNALRHTIYPNVEEWPRSDHSSLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDSTEKEAPFEPDNKPNKFWFSIEGTGALPAORIVTWGIGILKRKLEELNWALSNELO
AHAQOHILIFHFVKKHTSYNTAFFSONWVCGDCEKKLTKIVGVDPYRNKKVNRNADGS
GPKTVTTKNRLIGVOKKATIVGAKCKLCKMLIHQPGSHYCSTCAYOKGICAMCGKKIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MPGKECVIVLESVILHNFKMKFNFSFDKITCDTHFRLHLS
VKKTQYLEYFPNNGNMYNCLLYCTMCLDIFSSNSCISDVFNSNIPIMMICIASLMVIQ
                                                                                                                                                                                                                                                                /note="similar to DNA directed RNA polymerase II; cDNA EST EMBL:T00665 comes from this gene; cDNA EST EMBL:T01799 comes from this gene; cDNA EST EMBL:T01866 comes from this
             ATGRGEKPVREYLEEQYSEENTVDEATTLKLVVKSLAQVVPPGSQNIEIAVMKKVNDE
LQQRVLSTEEIEALLKVVETERVAAEAEEAASKKK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(20092. .20199,20247. .20454,20533. .20763,
21060. .21177,21227. .21384,21441. .21720,21763. .21900,
21967. .22119,22185. .22271))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to U4/U6 small nuclear ribonucleoprotein"
/codon_start=1
                                                                                                                                  15333. 15455,15510. 15644,15692. 15817,15970. .1
.16355,16401. 16524,16659. 16865,16912. .16963,
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EMBL:D72539 comes from this gene; cDNA EST EMBL:D75436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(18732. .19246)
/gene="C3681.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VIMESFPCVKDRSVKKMECSIDCCSIFSVLLNIARMVMFGG"
complement(20092. .22271)
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/gene="C36B1.7"
join(22786. .2295
                                                                                                                                                                                                            17223. .17327)
/gene="C36B1.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18732. .19246
/gene="C36B1.6"
                                                                                                              /gene="C36B1.3"
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/gene="C3581.1"
/note="CDNA EST EMBL:D34750 comes from this gene"
dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

This sequence is the entire insert of clone C36B1. The true right end of clone F38H1 is at 1799B in this sequence. The start of this sequence (1. 110) overlaps with the end of sequence 281079. The end of this sequence (44893. .44996) overlaps with the start of sequence 296047.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="mietgsgyllfllelficslfnsgstalqhedrvpnapqnvriktg
STSATLwwdappdptvlirgytveygegsisqriliegpdstsftvtrlspntnyvfa
VSAYneaegedgtkvwvaaktrpsegsgteklwpptsvrarideksaagsafvswddp
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GVEKKSIPALQDDRTIRKIHMIDDHVMLAFAGLSADARVLVDRARIECQSYKLTLEDP
VTVAYISRYIANTKQRFTQSPGRRPFGISMLIGGFDHDGTPRLFKTEPSGAXYEXVAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NPESSSENSIDSTOKOYVINYGIYESDTOOKVRSNAKAVRLTGLIPGKEYEVAVKVVA
GDGRESPWSIRDLFLVPETKTVSKFDWFCRLNDTEMCSIHSSPHWKLCSEKHDTYTOR
DAGACPRVQYPSSPAHLTTPAINLPDAQRLCLYFRFALLNFHPGQMKVEIFRDGDMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MLLPRHHLGGLLYFCALYLLRASQAQPPTFFALNALPGDSETEV
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TQFALEVVDQTVTFYFKCRRFASRQVTSLPDFSFDEAEKLYIASSAGPIIDNGFEVSLF
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/codon_start-1
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                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Caenorhabditis elegans"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:6239"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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                                                                                                                                   /gene="c36Bl.8"
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Hawkins,T.L., Birren,B.W., Fasman,K.H., Nussbaum,C., Lander,E.S., McKernan,K., Munro,C., Richardson,P., Barna,N., Chang,A., Cooke,P., Daly,M.J., Devon,K., Dewar,K., Forrest,C., Gage,D., Geraigery,K., Magos,B., Huang,J., Hul,L., Jacotot,L., Kirby,A., Lane,M., MacKenzie,J., Marquis,N., McDermott,J., Molla,M., Morrow,J., Nachman,A., Naylor,J., Nusbaum,C., O'Connor,T., Olotu,A., Peterson,K., Reeve,M.P., Roberts,D., Rollins,G., Stilwell,J., and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (122-AUG-1997) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jan 20, 1998 this sequence version replaced gi:2772532. The Staden databases, finishing information, and all chromatographic files used in the assembly of this clone are available from our anonymous ftp site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalla; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 91638)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-JAN-1998
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n, P. (1996–1997)
                                                                                                                                                                                                                                                                                                                                                 Gaps
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*NOTE: This is a 'working draft' sequence. It currently
*consists of 8 contigs. The true order of the places
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* tuns of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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                                                                                                                                                                                                                                                                                                  Score 26; DB 21; Length 44996; Pred. No. 4.43e+00;
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                                                                                                                                                                                                                                                                                                                                              4; Indels
                                                                                           AEVSSENSEIFEENGLKFEFCKWKVVENH"
23636. .28511
                                                                                                                                                                                                                                                                                                                                                                                      Db 36007 TTATTTGCAATTTTTTGCAGAAAGTTTTTAAA 36040
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Unpublished
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                                                                                                                                                                                                                                                     of annotations omitted.
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AC002489.1 GI:2795820
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Local Similarity 88.2%;
les 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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Note: remainder
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REFERENCE
AUTHORS
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JOURNAL
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Direct Submission
Submitted (27-AUG-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Aug 27, 1998 this sequence version replaced gi:3212897.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTICE: This sequence may not represent the entire insert of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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Homo sapiens BAC clone RG332B22 from 7p15-p21, complete sequence.
AC005094
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 158078)
Edwards,J. and Ozersky,P.
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C (bases 1 to 158078)
Waterston, R.H.
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/db_xref="taxon:9606"
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/map="X"
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AC005094.1 GI:3478660
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Best Local Similarity 88.2%;
Matches 30; Conservative
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MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 mapping project (Exic D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GIB/CHR7, send mailto:egreen@nhgri.nih.gov or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                    Clone RG332B22 is from the first release of the human BAC library CITB-978SK-B. The library contains cloned DNA from the male fibroblast cell line 978SK. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8 (1996). This clone is available from Research Genetics, Inc. VECTOR: pBeloBAC11
such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The clone sequenced to the right is RG023M10, 200 bp overlap. Actual start of this clone is at base position 1 of RG332B22; actual end is at 21981 of RG023M10.

Location/Qualifiers
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/clone="RG332B22"
complement(4183. .4302)
/db_ref="G1:454632"
5685. .5888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .158078
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17053. 17133
/rpt_family="MaLR"
17157. 17290
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rpt_family="MER81"
5150. .15521
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6316. .6774
/rpt_family="L1"
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8815. _9124
/rpt_family="Alu"
9384. .9440
/rpt_family="MIR"
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/rpt_family="MIR"
7454. .7659
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6749. .17049
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rpt_family="Alu"
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747. .8012
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795. .12068
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/rpt_famly="MERl_type" 26317 . 26548 /rpt_famlly="MIR" 27048 . .27148
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38733. .39032
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25430. .2580F
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23876. 2400-
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24222. . 25007
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39426. .39706
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/rpt_family-"Alu"
17617. .17896
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37449, 37744
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37745, 37983
                                                /rpt_family~"MaLR"
19068. .19369
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19842. .2001
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33055. .33407
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21967. .22200
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25991. PART
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7169. .27432
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/rpt_family="L2"
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35993. 247.
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36393. .37446
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1. (bases) to 198526)
Hyman, R.W., Fung, E.L., Qin, F., Tamaki, T., Kurdi, O.B. and Davis, R.W. Direct Submission
Direct Submission
Submitted (05-JAN-1999) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            malaria parasite P. falciparum.
Plasmodium falciparum
Eukaryota: Alveolata: Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 198526)
Hyman, R.W., Fung E.L., Qin, F., Tamaki, T., Kurdi, O.B. and Davis, R.W.
Plasmodium falciparum 3D7 chromosome 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC006280 198526 bp DNA HTG 05-MAR-1999
Plasmodium falciparum 3D7 chromosome 12 PFYAC724 genomic sequence,
WORKING DRAFT SEQUENCE, 9 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On Mar 5, 1999 this sequence version replaced g1:4176339.

* NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                     Length 158078;
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                                                                                                                                                                                                                                                                                                                                                                                  9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 26; DB 31;
Pred. No. 4.43e+00;
                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
41284. .41544
/rpt_family="MIR"
/rpt_family="Ale
/rpt_family="Ale
4225. .4268
/rpt_family="MalR"
4281. .4353
/rpt_family="MalR"
/rpt_family="MalR"
/rpt_family="MalR"
/rpt_family="MalR"
/rpt_family="MalR"
/rpt_family="MalR"
                                                                                                                                                                                                                                                                              Note: remainder of annotations omitted
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AC006280.2 GI:4337163
HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                     Query Match 22.8%;
Best Local Similarity 79.5%;
Matches 35; Conservative
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DEFINITION
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VERSION
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TITLE
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/Organism="Plasmodium falciparum"
/db_xref="taxon:583"
/chromosome="12"
/c
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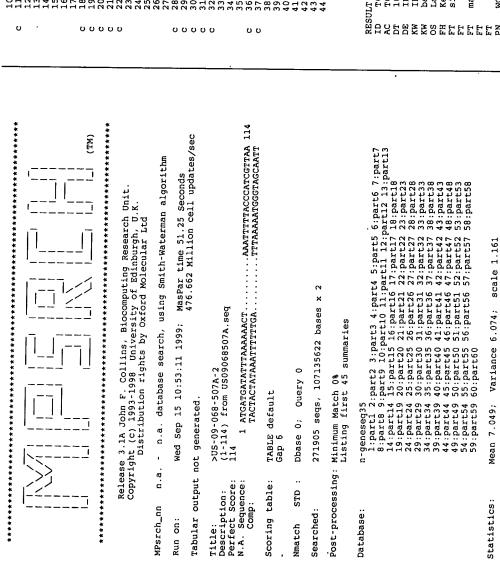
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Search completed: Wed Sep 15 10:47:20 1999 Job time : 544 secs.

13 AAAAAACTITCAGAAAAAGAATIGCAAAAAAAAAA 48

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18tics: Mean 7.049; Variance 6.074; scale 1.161

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		h DB ID Description Pred. No.		7.7.7	051746 Oligonucleotide probe	1 45 V44550 Marman 1 4	Manualtan DNA replica	9 Q51746 Oligonucleotide probe	TOTAL STORES	I Nollo4 Base substituted E.co	1 N81164 Page cubetituted p oc	Transcription Properties Properties	3 NSUU24 Sequence encoding new	HOW SWITTED COLUMN TO THE TAX OF	40 v44050 Mammallan DNA replica	3 N50023 Segmente encoding
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ALIGNMENTS

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Gene expression system providing regulated lactic acid bacteria protein production - uses new inducing peptide involved in bacteriocin synthesis, useful in fermentation and as a drug delivery
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This DNA sequence comprises the IF gene of Lactobacillus sake
LTH673 that encodes a secreted peptide (see W17988) which
autoinduces the expression of the IF-K-R gene cluster involved in
sakacin C production. The invention relates to the discovery of a
new regulatory mechanism for gene expression in lactic acid
                        10-DEC-1997 (first entry)
IF gene for bacteriocin-inducing peptide.
IF gene; gene expression; promoter; lactic acid bacterium; bacteriocin; vector; ss.
Lactobacillus sake strain LTH 673,
                                                                                                                                                                              /product- mature IF peptide
                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                              (BRUK) BRURBERG M B.
(EIJS/) EIJSINK V G H.
(NESI) NES I F.
Brurberg MB, Eijsink VGH, Nes IF;
WPI; 97-289292/26.
T67141 standard; DNA; 114 BP.
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/*tag= a
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22-MAY-1997.
13-NOV-1996; NO0266.
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                                                                                                                                               mat_peptide
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06-0CT-1998 (first entry)
Mammalian DNA replication origin consensus sequence, unforsconsensus.
DNA replication origin; human; mammal; alphaconsensus; unforsconsensus; anti-gene; DNA replication inhibitor; shuttle vector construct creation;
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bacteria that includes previously unrecognised, strongly regulatable promoter elements (see T67142-48). Expression of genes under the control of such promoters is dependent upon expression of the IF-K-R gene cluster or an analogue. Thus, the expression of a gene under the control of the promoter element in cells that gene under the control of the promoter element in cells that contain the K and R genes can be induced at will by adding the cognate, synthetic (harmless) inducing peptide. A recombinant vector containing the gene expression system, and host cells transformed with this vector, incorporated in the chromosome, and/or having integrated into its chromosome a promoter linked to an integrated gene encoding a specific protein are claimed. Typical applications are in fermentations (e.g. where the gene for menzyme is regulated and production of specific proteins, or where the bacteria express a surface antigen, as vaccines. Sequence 114 BP; 50 A; 12 C; 16 G; 36 T;
                                                                                                                                                                                                                                                                                                                                                                                 1 atgatgatatttaaaaaactttcagaaaaagaattgcaaaaaaataaacggtggtatggca 60
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oligonucleotide probe MXI4-A consists of nucleotides 5-95 of MXI4 (Q51735). It hybridized to all spp. of mycobacteria tested, but cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. see also Q51735-45 and Q51747-59.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ggaaatagttctaattttattcataagattaaacaaatttttacccatcgttaa 114
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Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New oligo:nucleotide probes specific for Mycobacteria - used detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                          DB 34; Length 114;
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                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 30; DB 9; Length 91;
Pred. No. 8.34e-03;
39; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GATGATATTTAAAAACTTTCAGAAAAAGAATTGCAAAAAATAAACGG 50
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                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                            Score 114;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 14; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     V44650 standard; DNA; 91 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q51746 standard; cDNA; 91 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-MAY-1993; 108325.
26-MAY-1992; US-889651.
(BECT ) BECTON DICKINSON CO.
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                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%;
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Mammalla.
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WPI; 93-378844/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 BP;
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01-DEC-1993.
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This sequence of the Invention, designated uniorsconsensus.

Consensus sequences of the Consensus sequence or an anti-gene (comprising a dual stranded copy of the consensus) is used to inhibit DNA replication of the vivo or in vitro. The consensus sequences can also be inserted into an expression vector, used subsequently for in vitro transfection of expression vector, used subsequently for in vitro transfection of control initiation of DNA replication. They can also be used used to maintain circular plasmids that are capable of semi-conservative replication in proliferating mammalian cells, or inserted into mammalian or human artificial chromosomal function. The consensus sequence can be considered for maintenance of corromosomal function. The consensus sequence can be considered with cloned human telomeres and large centromeric blocks for assembly of human artificial chromosomes and maintained as bacterial plasmids, circular or incart, large or small yeast artificial chromosomes (YACs) or as episomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 twaakrawrwwkkdavwwgakrwwkwvwhrassacmdwkaaktwkggwtwarrywkgrkm 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 TAAAAATTTGTTTAATCTTATGAATAAAATTAGAACTATTTCCTGCCATACCACGGTTTA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                       Human or mammalian origin of replication consensus sequences - for inhibiting DNA replication, for controlling initiation of replication, maintaining circular plasmids and in assembly of human artificial chromosomes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oligonuclectide probe MX14. A consists of nucleotides 5-95 of MX14 (Q51735). It hybridized to all spp. of mycobacteria tested, but cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New oligo:nucleotide probes specific for Mycobacteria - used for detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-YAY-1994 (first entry)
Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47; Mismatches 29; Indels
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                                                                                                     Cossons NH, Nielsen TO, Price GB, Zannis-Hadjopoulos M; WPI; 98-362770/31.
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C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 14; 23pp; English.
                                                                                                                                                                                                                                    Claim 1; Page 42; 54pp; English.
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Q51746 standard; cDNA; 91 BP.
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sest Local Similarity 13.6%;
fatches 12; Conservative
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EP-571911-A.
01-DEC-1993.
24-MAY-1993; 108325.
26-MAY-1992; US-889651.
                                   12-DEC-1997; CA0972.
21-MAY-1997; US-047322.
16-DEC-1996; US-033374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shank DD, Spears PA; WPI; 93-378844/48.
                                                                                               (UYMC-) UNIV MCGILL.
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366 baarmgdtaytayggnmgdathytbcaytayytbaatgcnaargattaywnncatt 421
        30-MAR-1988; 105163.
03-APR-1987; US-034819.
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                                                                                                                                                                                                                                                                                                        WPI: 88-279927/40.
Introducing random point mutations into nucleic acods -
Introducing random point mutations into nucleic acods -
By prepn of single stranded template, annealing a primer, elongation,
misincorporation, completion of molecules and screening.
Disclosure; p; English.
Random point mutations were introduced into the alpha fragment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 thhyrrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddhyvybbbvynvhnhnn 150
        Gaps
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                                                                                                   N81164;
08-NoV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
Escherichia coli.
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Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
Escherichia coli.
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0; Conservative 40; Mismatches 10; Indels 0;
                                                                                                                                                                                                                                                                                              Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T;
                     11 ssvhsyyvvhvvshhhsvhhvvhhvhvsvvvhhvvhhvhyhvysv 60
                                      106 GGGTAAAAATITGTITAATCTIATGAATAAAATIAGAACTATITCCTGCC 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.4%; Score 29; DB 1; Length 204; 8.0%; Pred. No. 2.10e-02;
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                                                                                                                                                                                         /*tag= a
/*taction=multiple cloning site
187..204
/*tag= b
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/*tag= b
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                                                                                                                                                                   Location/Qualifiers
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                                                                                           N81164 standard; DNA; 204 BP.
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8; Conservative
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03-APR-1987; US-034819.
(SUSO) SUOMEN SOKERI OY
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(SEAR ) SEAR D & CO.
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                                                                                                                                                 Introducing random point mutations into nucleic acods -
by prepn of single stranded template, annealing a primer, elongation,
misincorporation, completion of molecules and screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 29; DB 1; Length 204;
Pred. No. 2.10e-02;
47; Mismatches 42; Indels 0; Gaps
                                                                                                                                                                                                                                                                                        Disclosure; p; English.
Random point mutations were introduced into the alpha fragment of E.coll beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonucleotide was hybridised to to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can amplified and then expressed in a suitable tost-vector system. The sequence covers all 176 difft base substitutions, most of which covered and the molecules are offered to forms that can be sequence covers all 176 difft base substitutions, most of which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 Others;
(SUGO) STOWEN SOKERI OY.
Lehtovaara P, Knowles J, Kolvula A, Bamford J, Reinikainen T;
WPI; 88-279927/40.
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Pred. No. 5.26e-02;
15; Mismatches 16; Indels
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Local Similarity 10.1%;
hes 10; Conservative
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Local Similarity 44.6%;
nes 25; Conservative
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/*tag= a
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17-MAY-1984; GB-012564.
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17-MAY-1984; GB-012564.
                                                           P-PSDB; P50022
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 Human or mammalian origin of replication consensus sequences - for inhibiting DNA replication, for controlling initiation of replication, maintaining circular plasmids and in assembly of human prartificial chromosomes

PT artificial chromosomes

PT artificial chromosomes

Claim 1; Page 42; S4pp; English.

CC consensus sequence represents a human or mammalian DNA replication origin

CC consensus sequences of the invention, designated uniorsconsensus.

CC double stranded copy of the consensus sequence or an anti-gene (comprising a double stranded copy of the consensus is used to inhibit DNA replication

CC double stranded copy of the consensus sequences can also be inserted into an expression vector, used subsequently for in vitro transfection of control initiation of DNA replication. They can also be used used to maintain cricular plasmids that are capable of conservative replication in proliferating mammalian cells, or semi-conservative replication in proliferating mammalian cells, or semi-conservative replication in proliferating mammalian cells, or consensus sequence can be combined with cloned therapy. Particularly, they are used to create shuttle vector constructs for defining the essential mammalian elements required for maintenance of cromosomal function. The consensus sequence can be combined with cloned human telomeres and large centromeric blocks for assembly of human collinear, large or small yeast artificial chromosomes (YACs) or as episomal
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                                                                                                           06-OCT-1998 (first entry)
Mammalian DNA replication origin consensus sequence, uniorsconsensus.
DNA replication origin; human; mammal; alphaconsensus; uniorsconsensus; anti-gene; DNA replication inhibitor; shuttle vector construct creation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 mtwaakrawrwwkkdavwwgakrwwkwvwhrassacmdwkaaktwkggwtwarrywkgrk 62
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Best Local Similarity 12.9%; Pred. No. 1.31e-01;
Matches 11; Conservative 50; Mismatches 22; Indels 2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence encoding new modified human beta interferon polypeptides
   Antiviral; cell growth regulator; immune system regulator; antiproliferative; ss.
                                                                                                                                                                                                                                                          16-DEC-1996; US-033374.
(UYMC-) UNIV MCGILL.
Cossons NH. Nielsen TO, Price GB, Zannis-Hadjopoulos M;
WPI; 98-36270/31.
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                                                                               V44650 standard; DNA; 91 BP
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/*tag= a
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12-DEC-1997; CA0972.
21-MAY-1997; US-047322.
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17-MAY-1985; 105750.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 BP;
                                                                                                                                                                         gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                 V44650;
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                                                                    RESULT
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C.5-AR.1995 (first entry)
Generic DNA sequence to generate a random TSAR petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
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Claim 28; Chart 2d, page 35; 71pp; English.
Compared with interferon beta prepd. by recombinant methods, the INRS of the invention are more active and have different affinities for call surface receptors (allowing selective targetting); they have higher therapeutic index; improved stability against microbial breakdown during synthesis; and better in vivo solubility and stability. They are selected to recover from incubation mixts. Sequence 501 BP; 108 A; 31 C; 70 G; 81 T;
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                                                                                                                                    New modified human beta interferon polypeptide(s) - prepd. by plasmid transformed bacteria, with improved antiviral, anti-proliferative and immune requialting actions anti-proliferative and immune requialting actions (laim 28; Chart 2a, page 32; 71pp; English. Compared with interferon beta prepd. by recombinant methods, the INRS of the invention are more active and have different affinities for cell surface receptors (allowing selective targetting); they have higher therapeutic index; improved stability against microbial breakdown during synthesis; and better in vivo solubility and stability. They are selected to recover from incubation mixts. Sequence 501 Bp; 107 A; 31 C; 69 G; 80 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-SEP-1991 (first entry)
Sequence encoding new modified human beta interferon polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antiviral; cell growth regulator; immune system regulator; antiproliferative; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.8%; Score 26; DB 3; Length 501;
41.1%; Pred. No. 3.21e-01;
rative 16; Mismatches 17; Indels
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Bell LD, Boseley PG, Porter AG;
WPI; 85-311944/50.
P-PSDB; P50025.
(SEAR ) SEARLE G D & CO.
Bell LD, Boseley PG, Porter AG;
WPI; 85-311944/50.
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N50026 standard; DNA; 501 BP.
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nes 23; Conservative
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17-MAY-1984; GB-012564.
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11-DEC-1985
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PR 30-DEC-1993; US-013416.

PR 31-AN-1994; US-195506.

PR 31-AN-1994; US-198331.

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Pred. No. 1.89e+00;
27; Mismatches 76; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 GGGTAAAAATTTGTTTAATCTTATGAATAAAATTAGAACTATTTCCTGCCATACCACGGT 47
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effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss. Synthetic.
                                                                                                                                /*tag= a
/note= "this sequence represents '2'; Z can be
sequence of 6, 9 or 12 nucleotides (see
comments)"
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N50034 standard; DNA; 498 BP.
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Best Local Similarity 2.8%;
Matches 3; Conservative
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04-SEP-1991 (first entry)
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01-FEB-1994;
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                                                                                                          misc_feature
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17-MAY-1985; 105750.

18 17-MAY-1984; GB-012564.

19 (SEAR SEARLE G D & CC.

19 Bell LD, Boseley PG, Porter AG;

19 WIL, 85-311944/50.

18 WIL, 85-311944/50.

19 PSDB; P5003.

19 PSDB; P5003.

19 Pasmid transformed bacteria, with improved antiviral, anti-proliferative and immune regulating actions

19 Pasmid transformed bacteria, with improved antiviral, anti-proliferative and immune regulating actions

10 ST Compared with interferon beta prepd. by recombinant methods, the compared with interferon beta prepd. by recombinant methods, the compared with interferon are more active and have different affinities

10 Compared with interferon are more active and have different affinities

11 NRS of the invention are more active and have different affinities

12 for cell surface receptors (allowing selective targetting); they have higher therapeutic index; improved stability against microbial contents and better in vivo solubility and stability. They are also easier to recover from incubation mixts.

12 Sequence 498 BP; 112 A; 30 C; 68 G; 77 T;
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Claim 28; Chart 21, page 41; 71pp: English.
Compared with interferon beta prepd. by recombinant methods, the INFS of the invention are more active and have different affinities for cell surface receptors (allowing selective targetting); they have higher therapeutic index; improved stability against microbial breakdown during synthesis; and better in vivo solubility and stability. They are 108 A; 30 C; 72 G; 79 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363 baarmgdtaytayggnmgdathytbcaytayytbaargcnaargartaywnncayt 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 TAAACGGTGGTATGGCAGGAAATAGTTCTAATTTTTATTCATAAGATTAAACAAATT
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Pred. No. 1.89e+00;
16; Mismatches 18; Indels
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Best Local Similarity 39.3%; Pred. No. 1.89e+00;
Matches 22; Conservative 16; Mismatches 18
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17-MAY-1985; 105750.
17-MAY-1984; GB-012564.
(SEAR ) SEARLE G D & CO.
Bell LD, Boseley PG, Porter AG;
WPI; 85-311944/50.
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N50032 standard; DNA; 501 BP.
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21.1%;
Best Local Similarity 39.3%;
Matches 22; Conservative
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04-SEP-1991 (first entry)
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04-SEP-1991 (first entry)
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WHI: b3-31-31, ...
WHI: b3-31-31, ...
New modified human beta interferon polypeptide(s) - prepd. by plasmid transformed bacteria, with improved antiviral, anti-proliferative and immune regulating actions
claim 28: Chart 2k, page 42: 71pp: English.
Compared with interferon beta prepd. by recombinant methods, the INFs of the invention are more active and have different affinities in cell surface receptors (allowing selective targetting); they have higher therapeutic index; improved stability against microbial breakdown during synthesis; and better in vivo solubility and stability. They are also easier to recover from incubation mixts. Sequence 501 BP; 111 A; 31 C; 68 G; 80 T;
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Sequence encoding new modified human beta interferon polypeptides
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Sequence encoding new modified human beta interferon polypeptides
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                                                         Antiviral; cell growth regulator; immune system regulator; antiproliferative; ss.
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Pred. No. 1.89e+00;
16; Mismatches 18; Indels
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                                                                                                                                            Location/Qualifiers
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/*tag= a
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Bell LD, Boseley PG, Porter AG;
WPI; 85-311944/50.
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Bell LD, Boseley PG, Porter AG;
WPI; 85-311944/50.
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N50033 standard; DNA; 501 BP.
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Best Local Similarity 39.3%;
Matches 22; Conservative
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17-MAY-1985; 105750.
17-MAY-1984; GB-012564.
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17-MAY-1985; 105750.
17-MAY-1984; GB-012564.
                                                                                                                     Homo sapiens.
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Search completed: Wed Sep 15 10:54:09 1999 Job time : 58 secs.

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Scoring table:

Perfect Score: Sequence:

N.A.

Gap 6

1 ATGATGATATTTAAAAACT........AAAITTTTACCCATGGTTAA 114
TACTACTATAAAATTTTTGA.....TITAAAAATGGGTAGCAATT

Minimum Match 0% Listing first 45 summaries Post-processing:

n-issued 1:5A_COMB 2:5B_COMB 3:5C_COMB 4:PCT9_COMB 5:backfiles1 Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 6.588; Variance 4.618; scale 1.427

Statistics:

1.41e-03 3.36e-01 3.36e-01 9.62e-01 9.62e-01 9.62e-01 9.62e-01 9.62e-01 9.62e-01 9.62e-01 2.71e+00 2.71e+00 2.71e+00 2.71e+00 2.71e+00 2.71e+00 2.71e+00 Sequence 14, Application Sequence 27, Application Sequence 27, Application Sequence 4, Application Sequence 4, Application Sequence 37, Application Sequence 6, Application Sequence 10, Application Sequence 11, Application Sequence 12, Application Sequence 13, Application Sequence 14, Application Sequence 15, Application Sequence 25, Application Sequence 26, Application Sequence 26, Application Sequence 26, Application Sequence 26, Application Sequence 27, Application Sequence 27, Application Sequence 27, Application Sequence 27, Application Sequence 21, Application Sequence 10, Application Description PCT-US91-0 US-08-471-SUMMARIES Match Length DB 7218 33440 34440 10090 110090 110090 110090 110091 10091 Result O

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Ann i catto	ייייייייייייייייייייייייייייייייייייייי	Applicatio	Applicatio	Applicatio	Application	Application	ייייייייייייייייייייייייייייייייייייייי	Applicatio	Applicatio	5510472	Application	Application	01101111111	Applicatio	Applicatio	Application	2001400400	חדום הדהללט	Applicat1	Applicati	Applicatio	Application	011111111111111111111111111111111111111	Applicatio	Applicatio	Application	חייים	Appilcatio	Applicatio	Applicatio	
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US-08-188-	115-08-140-	, ,		7-0	US-08-377-	US-08-188-	DOM-HOD	0-0660 104	US-08-480-	5510472-1	US-08-440-	US-08-482-	115-08-369-		05-08-482-	US-08-368-	US-08-081-	1-0001-000	1 2 6 6 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5	-166-10-50	US-07-991-	US-08-107-	0-9051-100	0.000 103	2	US-08-101-	2	000	-01-99	US-08-323-	
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ALIGNMENTS

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Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
Septement No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F. APPLICANT: SCHEIFLINGER, F. APPLICANT: FLANDER, F. G. TITLE OF INVENTION: RECOMBINANT FOWLDOX VIRUS NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS: ADDRESSEE: FOLEY & LARGHER STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                            COUNTRY: USA

ZIF: 22313-0299

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFENCE/COCKET NUMBER: 30472/114 IMMU
TELEPHONE: (703)836-9300
TELEPA: (703)836-9300
TELEX: (703)836-9300
TELEX: (703)836-9300
TELEX: (703)836-9300
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
US-08-232-463-14 STANDARD; DNA; UNC; 7218
                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                       STREET: 1800 Diac
CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
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Gaps
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                                IMMEDIATE SOURCE:
CLONE: pTZgpt-F1s
SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.3%; Score 22; DB 1; Length 2183
80.6%; Pred. No. 3.36e-01;
vative 0; Mismatches 7; Indels
                                                                     23.7%; Score 27; DB 2; Length 7218; Similarity 3.4%; Pred. No. 1.41e-03; 2; Conservative 41; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MMEDIATE SOURCE:
CLONE: 1.5 Kb Clai fragment from fowl pox virus
CLONE: 1.5 Kb Clai fragment from fowl pox virus
CLONE: 1.5 Kb Clai fragment from fowl pox virus
SEQUENCE 2183 BP; 736 A; 326 C; 292 G; 829 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/993,073
FILING DATE: 19921218
CLASSIFICATION: A35
                                                                                                                                                                                                                                                                                                                                                                                                                     CLARESTRICATION:
ACTURATION:
NAME: KOWALCHYK, Alan W.
REGISTRATION NUMBER: 31,535
REFERENCE/DOCKET NUMBER: 6159.197-US02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-530
TELEPAX: 612-332-59081
INFORMATION FOR SQL ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2183 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1882 AAATACTTCTTACTTAATTCATAAAATTCAATAAAT 1917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/07993073
Sequence 1, Application US/07993073
Sequence 1, Application US/07993073
Patent No. 5386855
GENERAL INFORMATION:
APPLICANT: Boyle, David B.
APPLICANT: Kumar, Sharad
TITLE OF INVENTION: Pox Virus Vectors
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                             T
US-07-993-073-1 STANDARD; DNA; UNC; 2183 BP
                                                                                                                                                                                                                                                                               ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5368855west Center
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA (genomic)
LENGIH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 80.6%;
Matches 29; Conservative
        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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Gaps
                                                                           Sequence 27, Application PC/TUS9101746
Sequence 27, Application PC/TUS9101746
GENERAL INFORMATION:
APPLICANT: Thompson, Gregory A
APPLICANT: Redué, Vic C
TITLE OF INVENTION: Plant Desaturases-Compositions and Uses
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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Best Local Similarity 78.9%; Pred. No. 3.36e-01;
Matches 30; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
SEQUENCE 3440 BP; 1165 A; 668 C; 540 G; 1067 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 27, Application US/08471791
Sequence 27, Application US/08471791
Patent No. 5723595
Patent No. 15723595
Patent No. FORMATION:
APPLICANT: Thompson, Gregory A
APPLICANT: Thompson, Usc.
TITLE OF INVENTION: Plant Desaturases-Compositions
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2306 TITCTITITGAAATTITITITITGAAATTITITGAA 2343
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US-08-471-791-27 STANDARD; DNA; UNC; 3440 BP.
7. 3
PCT-US91-01746-27 STANDARD; DNA; UNC; 3440 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLUM TIRE: DISKELLE, 3:00 LINCH, 1:00 COMPUTER: Apple Macintosh OPERATING SYSTEM: Macintosh 6:0.7 SOFTWARE: MicrosoftWord 4:0 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US91/01746 FILING DATE: 19910314 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/615,784 FILING DATE: 14-NOV-1990 APPLICATION NUMBER: 07/567,373 FILING DATE: 16-MAR-1990 APPLICATION NUMBER: 07/494,106 FILING DATE: 16-MAR-1990 ATTONNEY/AGENT INFORMARTOR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGNE 69-3 WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: CGNE TELECOMMUICATION INFORMATION: TELEPHONE: (916) 753-6313 TELEFAX: 35370 GGNE INFORMATION FOR SEQ ID NO: 27: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Lassen, Elizabeth
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGIH: 3440 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEIC ACID
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  XXXXXX
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CDNA to mRNA
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                                                                                   CITY: Princeton
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORANISM: Human
CELL LINE: HeLa
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL: Cell
                                                                     STREET:
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   Gaps
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                                                                                                                              ZIP: 955.05
ZUP: 9
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19.3%; Score 22; DB 2; Length 3440;
Best Local Similarity 78.9%; Pred. No. 3.36e-01;
Matches 30; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: genomic DNA
SEQUENCE 3440 BP; 1165 A; 668 C; 540 G; 1067 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2306 TITCITITIGAAAITITITITITIGAAAITITIGAA 2343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Mandel, Gail, Chong, Jayhong A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Lassen, Elizabeth
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERNCE/DOCKET NUMBER: GGNE 69-5
TELEPHONE: (916) 753-6313
TELEPHONE: (916) 753-1510
TELEFAX: (916) 753-1510
TELEFAX: 350370 GGNE
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JT 5
PCT-US96-03940-5 STANDARD; DNA; UNC; 928
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/615,784
FILING DATE: 14-NOV-1990
PRIOR APPLICATION NUMBER: 07/567,373
APPLICATION NUMBER: 07/567,373
FILING DATE: 13-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/494,106
FILING DATE: 16-MAR-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application PC/TUS9603940 Sequence 5, Application PC/TUS9603940 GENERAL INFORMATION:
TITLE OF INVENTION: and USES NUMBER OF SEQUENCES: 45 CORRESPONDENCE ADDRESS:
                                                 ADDRESSEE: Calgene, Inc. STREET: 1920 Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 3440 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                       CITY: Davis
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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ID PC
AC XX
DT XX
DE SE
CC SE
CC CC
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LIBRARY: CDNA
PUBLICATION INFORMATION:
AUTHORS: Chong, Jayhong A., Tapia-Ramirez Jos , Toledo-
AUTHORS: Aral, Juan, Zheng, Yingcong, Boutros, Michael C., Altschuler,
AUTHORS: Yelena M., Frohman, Michael A., Kraner, Susan D., Mandel, Gail
TITLE: REST: A Mammalian Silancer Protein that Restricts
TITLE: Sodium Channel Gene Expression to Neurons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                     COMPRY: New Jersey
COMPRY: New Jersey
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM-Compatible
OPERATING SYSTEM: DOS 5.0
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
RAPPLICATION NUMBER: PCT/US96/03940
FILING DATE: March 23, 1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 18.4%; Score 21; DB 4; Length 928; Best Local Similarity 74.4%; Pred. No. 9.62e-01; Matches 32; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RELEVANT RESIDUES IN SEQ ID NO: 5:FROM 1 TO 928 SEQUENCE 928 BP; 363 A; 178 C; 182 G; 205 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        643 CAGAAATAGAACAAAAAAAAAAAAAAAGGGGATGTGGCTGGAAA 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 CAGAAAAAGAATTGCAAAAAATAAACGGTGGTATGGCAGGAAA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application PC/TUS9603940
Sequence 4, Application PC/TUS9603940
GENERAL INFORMATION:
APPLICANT: Mandel, Gail, Chong, Jayhong A.
TITLE OF INVENTION: REST Protein and DNA
WUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .T 6
PCT-US96-03940-4 STANDARD; DNA; UNC; 1090 BP
TITLE OF INVENTION: REST Protein and DNA NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSE: Dechert Price & Rhoads
STREET: P.O. Box 5218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Allen Bloom
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-101
TELECOMMUNICATION INFORMATION:
TELEFAX: (609) 520-3214
TELEFAX: (609) 520-3259
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 928 base pairs
TYPE: nuclet acid
STRANDEDNESS: double
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STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  XXXXXX
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   LIBRARY: CDNA

PUBLICATION INFORMATION:

AUTHORS: Chong, Jayhong A., Tapia-Ramirez Jos , Toledo-
AUTHORS: Aral, Juan, Zheng, Yingcong, Boutros, Michael C., Altschuler,
AUTHORS: Relena M., Frohman, Michael A., Kraner, Susan D., Mandel, Gail
TILLE: REST: A Mammalian Silencer Protein that Restricts
TITLE: Sodium Channel Gene Expression to Neurons
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                                       COMPTRY: Now Jesus J. 1984 - 5218

ZIP: 0843-5218

COMPUTER READABLE Diskette, 3.50 inch, 1.44 Mb storage COMPUTER: IBM-compatible OPERATING SYSTEM: DOS 5.0

SOFTWARE: WordPerfect CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/03940

FILING DATE: March 23, 1995

CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 21; DB 4; Length 1090; Pred. No. 9.62e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DATE: March 24, 1995
RELEVANT RESIDUES IN SEQ ID NO: 4:FROM 1 TO 1090
SEQUENCE 1090 BP; 433 A; 206 C; 219 G; 232 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   702 CAGAAATAGAACAAACAAAATAAAAGGGGATGTGGCTGGAAA 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 CAGAAAAAGAATTGCAAAAAATAAACGGTGGTATGGCAGGAAA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application PC/TUS9603940
Sequence 3, Application PC/TUS9603940
Sequence 3, Application PC/TUS9603940
SEMERAL INFORMATION:
APPLICANT: Mandel, Gail, Chong, Jayhong A.
TITLE OF INFURION: REST Protein and DNA
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Allen Bloom
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 520-3214
TELEPHONE: (609) 520-3259
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1090 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT-US96-03940-3 STANDARD; DNA; UNC; 1407
ADDRESSEE: Dechert Price & Rhoads
STREET: P.O. Box 5218
CITY: Princeton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Dechert Price & Rhoads
STREET: P.O. Box 5218
CITY: Princeton
                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 18.4%;
Best Local Similarity 74.4%;
Matches 32; Conservative
                                New Jersey
: USA
                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                ORGANISM: Human
CELL LINE: HeLa
                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE: Sodiu
JOURNAL: Ce
VOLUME: 80
                                                                                                                                                                                                                                                                                                                           ANTI-SENSE:
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AUTHORS: Chong, Jayhong A., Tapia-Ramirez Jos, Toledo-AUTHORS: Aral, Juan, Zheng, Yingcong, Boutros, Michael C., Altschuler, AUTHORS: Aral, Juan, Zheng, Yingcong, Boutros, Michael C., Mandel, Gail TITLE: REST: A Mammallan Silencer Protein that Restricts
TITLE: Sodium Channel Gene Expression to Neurons
JOURNAL: Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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COUNTRY: USA
ZIP: 08543-5218
COMPUTER READALE FORM:
MEDIUM TYPE: DISKette; 3.50 inch, 1.44 Mb storage
COMPUTER: IBM-compatible
OPERATING SYSTEM: DOS 5.0
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/03940
FILING DATE: March 23, 1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 21; DB 4; Length 1407; Pred. No. 9.62e-01; 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DATE: March 24, 1995
RELEVANT RESIDUES IN SEQ ID NO: 3:FROM 1 TO 1407
SEQUENCE 1407 BP; 515 A; 276 C; 306 G; 310 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1122 CAGAAATAGAACAAACAAAATAAAAGGGGATGTGGCTGGAAA 1164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 27, Application PC/TUS9603940
Sequence 27, Application PC/TUS9603940
GENERAL INFORMATION:
APPLICANT: Mandel, Gail, Chong, Jayhong A.
TITLE OF INFUNINION: REST Protein and DNA
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .r 8
PCT-US96-03940-27 STANDARD; DNA; UNC; 1461 BP
                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Allen Bloom
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-101
TELECOMMUNICATION INFORMATION:
TELEFAHONE: (609) 520-3214
TELEFAHONE: (609) 520-3259
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1407 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Dechert Price & Rhoads
STREET: P.O. Box 5218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIBRARY: CDNA
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 18.4%;
Best Local Similarity 74.4%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Princeton
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Human
CELL LINE: HeLa
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08543-5218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: no
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VOLUME: 80
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Wed_Sep 15 12:54:05 1999

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LIBRARY: CDNA
PUBLICATION INFORMATION:
AUTHORS: Chong, Jayhong A., Tapia-Ram!rez Jos , Toledo-
AUTHORS: Aral, Juan, Zheng, Kingcong, Boutros, Michael C., Altschuler,
AUTHORS: Yelena M., Frohman, Michael A., Kraner, Susan D., Mandel, Gail
TITLE: REST: A Mammalian Silencer Protein that Restricts
TITLE: Sodium Channel Gene Expression to Neurons
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Sequence 10, Application PC/TUS9603940
CENERAL INFORMATION:
APPLICANT: Mandel, Gail, Chong, Jayhong A.
TILE OF INVENTION: REST Protein and DNA
TUTHE OF INVENTION: REST Protein and DNA
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSE: Dechert Price & Rhoads
STREET: P. D. Box 5218
CITY: Princeton
STREET: New Jersey
COUNTRY: USA
ZIP: 08543-5218
COMPUTER: READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM-compatible
COMPUTER: Machderfect
CURPRATING SYSTEM: DOS 5.0
SSCTWARE: Wardderfect
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DATE: March 24, 1995
RELEVANT RESIDUES IN SEQ ID NO: 6:FROM 1 TO 1791
SEQUENCE 1791 BP; 607 A; 395 C; 406 G; 383 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1512 CAGAAATAGAACAAAAAAAAAAAAGGGGATGTGGCTGGAAA 1554
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PCT-US96-03940-10 STANDARD; DNA; UNC; 3291 BP.
                                   SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/03940
FILLING DATE: MARCH 23, 1995
CLASSIFTCATION:
ATTONEY/AGENT INFORMATION:
NAME: Allen Bloom
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 31743-101
TELEPHONE: (609) 520-3214
TELEPHONE: (609) 520-3214
INFORMATION FOR SEG ID NO: 6: SEQUENCE CHRAATERISTICS:
LENGTH: 1791 base pairs
TYPE: nucleic acid
TYPE: Application of the control of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
                   OPERATING SYSTEM: DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Human
CELL LINE: HeLa
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL: CE
VOLUME: 80
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PUBLICATION INFORMATION:
AUTHORS: Chong, Jayhong A., Tapia-Ramirez Jos , Toledo-
AUTHORS: Anal, Zheng, Yingcong, Boutros, Michael C., Altschuler,
AUTHORS: Yelena M., Frohman, Michael A., Kraner, Susan D., Mandel, Gail
TITLE: REST: A Mammalian Silencer Protein that Restricts
TITLE: Sodium Channel Gene Expression to Neurons
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Pred. No. 9.62e-01;
0; Mismatches 11; Indels
                MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage COMPUTER: IBM-compatible ODERAING SYSTEM: DOS 5.0 SOFTWARE: WordPerfect CURREWY APPLICATION DATA: APPLICATION NUMBER: PCT/US96/03940 FLING DATE: March 23, 1995 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DATE: March 24, 1995
RELEVANT RESIDUES IN SEQ ID NO: 26:FROM 1 TO 1461
SEQUENCE 1461 BP; 528 A; 288 C; 326 G; 319 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM-compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1217 CAGAAATAGAACAAACAAAATAAAAGGGGATGTGGCTGGAAA 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 CAGAAAAGAATTGCAAAAATAAACGGTGGTATGGCAGGAAA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application PC/TUS9603940
Sequence 6, Application PC/TUS9603940
GENERAL INFORMATION:
APPLICANT: Mandel, Gail, Chong, Jayhong A.
TITLE OF INVENTION: REST Protein and DNA
NUMBER OF SEQUENCES: 29
CORRESPONDENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: P.O. Box 5218
CITY: Princeton
STATE: New Jersey
COUNTRY: USA
ZIP: 08543-5218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9

ID PCT-US96-03940-6 STANDARD; DNA; UNC; 1791 BP. Ac xxxxxx

DT Sequence 6, Application PC/TUS9603940

CC GENERAL INFORMATION:
CC GENERAL INFORMATION:
CC APPLICANT: Mandel, Gail, Chong, Jayhong A. TITLE OF INVENTION: REST Protein and DNA CC NUMBER OF SEQUENCES: 29

CC CORRESPONDENCE ADDRESS: 29

CC ADDRESSE: Dechert Price & Rhoads

CC CORRESPONDENCE ADDRESS: CC COUNTRY: Princeton

CC CITY: Princeton

CC CITY: Princeton

CC CITY: Princeton

CC COUNTRY: USA

CC COUNTRY: USA

CC COMPUTER READABLE FORM:
CC COMPUTER READABLE FORM:
CC COMPUTER IBM-compatible
                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Allen Bloom
REGISTRATION UNBER: 29,135
REFERENCE/DOCKET NUMBER: 21743-101
TELECOMMUNICATION INFORMATION:
LEGGRAPH 1461 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 74.4%;
Matches 32; Conservative
COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Human
CELL LINE: HeLa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  o
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE: Sodit
JOURNAL: Ce.
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Sequence 1, Application US/07841655
Sequence 1, Marugy, A.M. Ledeboer, P.A. Vandenbergh APPLICANT: and J.T. Henderson
TITLE OF INVENTION: Cloned Gene Encoding For Bacteriocin TITLE OF INVENTION: From Pediococcus acidilactici NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ian C. McLeod
STREET: 2190 Commons Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE: N-terminal, internal and C-terminal fragments ORIGINAL SOURCE: ORGANISM: Pediococcus acidilactici
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: bacteriocin encoding DNA
LOCATION: ECORI to Sall
LOCATION: DNA fragment 5.6 kbp.
IDENTIFICATION METHOD: sequencing
O'THER INFORMATION: DNA needed for bacteriocin expression.
PUBLICATION INFORMATION: N/A
SEQUENCE 5555 BP: 1759 A: 1007 C; 1006 G; 1823 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
18.4%; Score 21; DB 1; Length 5595;
Best Local Similarity 69.1%; Pred. No. 9.62e-01;
Matches 38; Conservative 0; Mismatches 17; Indels
            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MT 4.1-129
TELECOMUNICATION INFORMATION:
TELEFAX: (517) 347-4103
TEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .r. 12
US-07-841-655-1 STANDARD; DNA; UNC; 5595 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INDIVIDUAL ISOLATE: PAC1.0
DEVELOPMENTAL STAGE: N/A
                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: Linear
MOLECULE TYPE: Plasmid DNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANELLE: N/A
IMMEDIATE SOURCE: N/A
POSITION IN GENOME: N/A
FEATURE:
FILING DATE: 19911231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN: NRRL-B-18050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAPLOTYPE: N/A
TISSUE TYPE: N/A
CELL TYPE: N/A
CELL LINE: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Michigan
                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: NA ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 2190
CITY: Okemos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 48864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: J.D. Marugg, A.M. Ledeboer, P.A. Vandenbergh and J.T. Henderson TITLE OF INVENTION: Cloned Gene Encoding For Bacteriocin From TITLE OF INVENTION: Pediococcus acidilactici NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jan C. McLeod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIBRARY: CDNA
PUBLICATION INFORMATION:
AUTHORS: Chong, Jayhong A., Tapia-Ram!rez Jos , Toledo-
AUTHORS: Aral, Juan, Zheng, Yingcong, Boutros, Michael C., Altschuler,
AUTHORS: Yelena M., Frohman, Michael A., Kraner, Susan D., Mandel, Gail
TITLE: REST: A Mammalian Silencer Protein that Restricts
TITLE: Sodium Channel Gene Expression to Neurons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 21; DB 4; Length 3291;
Pred. No. 9.62e-01;
0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DATE: March 24, 1995
RELEVANT RESIDUES IN SEQ ID NO: 10:FROM 1 TO 3291
SEQUENCE 3291 BP; 1091 A; 694 C; 807 G; 699 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1337 CAGAAATAGAACAAACAAAATAAAAGGGGATGTGGCTGGAAA 1379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 CAGAAAAAGAATTGCAAAAATAAACGGTGGTATGGCAGGAAA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
ID US-07-635-965C-1 STANDARD; DNA; UNC; 5595 BP
                                                          ATTORNEY AGENT INFORMATION:
NAME: Allen Bloom
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-101
TELECOMMUNICATION INFORMATION:
TELECHOK: (609) 520-3214
TELEFRX: (609) 520-3259
INFORMATION FOR SEQ ID NO: 10:
SEGUENCE CHARACTERISTICS:
LENGTH: 3291 base pairs
TYPE: nucleic acid
STRANDEDNESS: Gouble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: ASCII text editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/635,965C
  APPLICATION NUMBER: PCT/US96/03940 FILING DATE: March 23, 1995 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/07635965C
Sequence 1, Application US/07635965C
Patent No. 2506212
GENERAL INFORMATION:
APPLICANT: J.D. Marugg, A.M. Lede
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Ian C. McLeod
STREET: 2190 Commons Parkway
CITY: Okemos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM AT OPERATING SYSTEM: MS-DOS 4.01
                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 18.4%;
Best Local Similarity 74.4%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Michigan
COUNTRY: USA
                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                               CELL LINE: HeLa
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                    2
                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: no
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL: Ce.
VOLUME: 80
ISSUE:
                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               xxxxxx
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AUTHORS: Juan, Zheng, Yingcong, Boutros, Michael C., Altschuler, Yelena AUTHORS: Juan, Zheng, Michael A., Kraner, Susan D., Mandel, Gail AUTHE: REST: A Mammalian Sileneer Protein that Restricts TILE: Sodium Channel Gene Expression to Neurons
                                                                                         ZUP: 1845-5218

ZUP: 1845-5218

ZUP: 1845-5218

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: BM-compatible
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Wardberfect
CURRATING SYSTEM: DOATA:
APPLICATION NUMBER: PCT/US96/03940
FILING DATE: March 23, 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Allen Bloom
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 29,135
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATICS:
LENGTH: 6609 520-3214
TELECAMONE CHARACTERISTICS:
LENGTH: 6648 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 18.4%; Score 21; DB 4; Length 5648; Local Similarity 74.4%; Pred. No. 9.62e-01; es 32; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RELEVANT RESIDUES IN SEQ ID NO: 1:FROM -1 TO 5648 SEQUENCE 5648 BP; 1747 A; 1098 C; 1294 G; 1507 T; 2 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIBRARY: CDNA
PUBLICATION INFORMATION:
AUTHORS: Chong, Jayhong A., Tapia-Ramirez Jos ,
AUTHORS: Toledo-Aral,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1661 CAGAAATAGAACAAACAAAATAAAAGGGGGTGTGGCTGGAAA 1703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 CAGAAAAAGAATTGCAAAAAATAAACGGTGGTATGGCAGGAAA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/08238163
Sequence 5, Application US/08238163
Patent No. 5569830
GENERAL INFORMATION:
APPLICANT: BENNETT, Alan
APPLICANT: LABAVITCH, John M.
APPLICANT: STOTZ, Henrik
TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
ID US-08-238-163-5 STANDARD; DNA; UNC; 215 BP.
               ADDRESSEE: Dechert Price & Rhoads STREET: P.O. Box 5218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA to MRNA
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DATE: March 24, 1995
                                                                 New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CELL LINE: HeLA IMMEDIATE SOURCE:
                                                 Princeton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: no
ORIGINAL SOURCE:
                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL: CE
VOLUME: 80
                                                                                  COUNTRY:
                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Local Similarity 69.1%; Pred. No. 9.62e-01;
nes 38; Conservative 0; Mismatches 17; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1076 ATGAAAAAATTGAAAATTAACTGAAAAAGAAATGGCCAATATCATTGGTGGTA 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: bacteriocin encoding DNA
LOCATION: ECORI to Sali
LOCATION: DNA LEGEBRE 5.6 kbp.
IDENTIFICATION METHOD: Sequencing
OTHER INFORMATION: DNA needed for bacteriocin
OTHER INFORMATION: expression.
PUBLICATION INFORMATION: N/A
SEQUENCE 5595 BP; 1759 A; 1007 C; 1006 G; 1823 T; 0 OTHER.
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE: N-terminal, internal and C-terminal FRAGMENT TYPE: fragments
ORIGINAL SOURCE:
ORGANISM Pediococcus acidilactici
STRAIN: NRRL-B-18050
INDIVIDUAL ISOLATE: PACL.0
DEVELOPMENTAL STAGE: N/A
            COMPUTER KALLADOLL. .....

COMPUTER: Diskette, 5.25 inch, 360 Kb COMPUTER: IBM AT OPERATING SYSTEM: MS-DOS 5.00

SOFTWARE: ASCII text editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/841,655
FILING DATE: 19910225
CLASSIFICATION TO ATA:
APPLICATION NUMBER: 07/635,965
FILING DATE: 19900
ATTORNEY/AGENT INFORMATION:
NAME: Lan C. McLeod
RECISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MT 4.1-140
TELEPHONE: (517) 347-4103
TELEPHONE: (517) 347-4103
TELEPHONE: (517) 347-4103
TELER: NO. 5175252e
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARRACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Mandel, Gail, Chong, Jayhong A. TITLE OF INTENTION: REST Protein and DNA WUMBER OF SEQUENCES: 29 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /T 13
PCT-US96-03940-1 STANDARD; DNA; UNC; 5648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application PC/TUS9603940
Sequence 1, Application PC/TUS9603940
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Linear MOLECULE TYPE: Plasmid DNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE: N/A POSITION IN GENOME: N/A
                                                                                                                                                                                                                                                                                                                                                                                              TYPE: NUCLEIC ACID
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAPLOTYPE: N/A
TISSUE TYPE: N/P
CELL TYPE: N/A
CELL LINE: N/A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE
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1 MINVIMSSSSVVSRTASCNDKAKKDGNTTSSWTTDCCNRTWGVCDTDTTYRVNNDS 56
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LOCATION: 1..215
OTHER INFORMATION: /standard_name= "Deduced amino acid
OTHER INFORMATION: sequence of PGIP from bean."
SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 17.5%; Score 20; DB 1; Length 215; Best Local Similarity 16.1%; Pred. No. 2.71e+00; Matches 9; Conservative 26; Mismatches 21; Indels
        SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,163
FILING DATE: 03-MAY-1994
CLASSIFICATION: 800
ATTONNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 2307E-540
TELEPHONE: (415) 543-9600
TELEPAS: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 base pairs
TYPE: nucleic acid
STRANDEDMESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: Wed Sep 15 10:38:57 1999 Job time : 19 secs.
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                              unknown
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 8888888888888888888888888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/08238163
GENERAL INFORMATION:
APPLICANT: BENNETT, Alan
APPLICANT: DOWELL, Annik
APPLICANT: STOTZ, Henrik
TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
 IIILE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ő
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 1..215
OTHER INFORMATION: /standard_name= "Deduced amino acid
OTHER INFORMATION: sequence of POIP from bean."
SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 17.5%; Score 20; DB 1; Length 215; Best Local Similarity 22.9%; Pred. No. 2.71e+00; Matches 8; Conservative 17; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco STATE: California
                                                                                                        COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATEMING SYSTEM:
SOFTWARE: PATEMIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,163
FILING DATE: 03-MAY-1994
CLASSIFICATION: 800
                                         ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 RTGKTANNAVDSRNMGDASVGSDKNTKKHAKNSAD 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 2307E-540
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFRA: (415) 543-9600
TELEFRA: (415) 543-5043
INFORMATION FOR SEO ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JT 15
US-08-238-163-5 STANDARD; DNA; UNC; 215 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94105-1493
COMPUTER REACABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown MOLECULE TYPE: protein
                NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancis
COUNTR: US
                                                                                           STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             XXXXXX
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Gaps

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~ Wed∹Sep 15 12:54:07 1999



Statistics: Mean 9.510; Variance 3.329; scale 2.857

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ				
esult		Query				
Š.	Score	Match	Match Length DB	QI -	Description	Pred. No.
-	31	27.2	252 17	AA754459	97SN1787 Rice Immature	3.636-08
7	30	26.3	2275 20	AF034173	AF034173 Human mRNA (T	
m	29	25.4	252 17	AA754459	97SN1787 Rice Immature	
4	25	21.9	365 24	AI267433	ad47e06.x1 Stanley Fro	4.01e-03
Ŋ	25	21.9	392 24	AI267345	ad46e06.xl Stanley Fro	
9	25	21.9	675 39	AQ083705	CPG0587A CPIOWAGDNA1 C	
7	24	21.1	356 40	AQ268382	RPCI11-69M19.TJ RPCI11	"
æ	24	21.1	359 18	AA764146	vv45d06.rl Soares 2NbM	
σ	24	21.1	423 25	AU039222	AU039222 Dictvostelium	
10	24	21.1	434 40	AQ268460	RPCI11-74G21.TJ RPCI11	•

24 21.1 435 24 AU033574 AU033574 Dictyostelium 2.45e-02 23 20.2 233 41 AO344881 RPCIII-11417.TJ RPCII 2.45e-02 23 20.2 233 11 AA34468 EST38697 Embryo, 9 wee 1.44e-01 23 20.2 293 11 AA34468 EST38697 Embryo, 9 wee 1.44e-01 23 20.2 349 27 AI47823 CEEKOZIHYR VONATE unp 1.44e-01 23 20.2 349 27 AI47823 CEEKOZIHYR VONATE unp 1.44e-01 23 20.2 349 27 AI47823 CEEKOZIHYR VONATE unp 1.44e-01 23 20.2 349 27 AI47823 CEEKOZIHYR VONATE unp 1.44e-01 23 20.2 349 27 AI47823 CEEKOZIHYR VONATE unp 1.44e-01 23 20.2 349 37 AI47823 CEEKOZIHYR VONATE unp 1.44e-01 23 20.2 340 37 AA748479 VOJEGOS.SI SOSTES DES L'44e-01 24 400 3 R50363 VOJEGOS.SI SOSTES DES 1.44e-01 25 20.2 441 8 B3226 CIT-HSP.31 NCI_CGAP_CG 1.44e-01 26 20.2 441 8 B3226 CIT-HSP.31 NCI_CGAP_CG 1.44e-01 27 20.2 441 8 B3226 CIT-HSP.31 NCI_CGAP_CG 1.44e-01 28 20.2 441 8 B3226 CIT-HSP.31 NCI_CGAP_CG 1.44e-01 28 20.2 542 22 AI066149 TRNUSSOL TO REPERT I.44e-01 29 20.2 542 22 AI066149 TRNUSSOL TO REPERT I.44e-01 20 20 244 A AQ375560 RPCIII-15072.TV RPCII 1.44e-01 21 20 2 612 41 AQ375560 RPCIII-15072.TV RPCII 1.44e-01 22 20 2 612 41 AQ375560 RPCIII-15072.TV RPCII 1.44e-01 23 20 2 612 41 AQ375560 RPCIII-15072.TV RPCII 1.44e-01 24 37 B12681 RPCIII-113020.TJ RPCII 1.44e-01 25 20 2 612 41 AQ375560 RPCIII-15040.TMR CIT 1.44e-01 26 20 3 63 AI557158 RPCIII-113020.TJ RPCII 1.44e-01 27 759 40 AQ25362 RPCIII-113020.TJ RPCII 1.44e-01 28 20 2 612 41 AQ37550 RPCIII-113020.TJ RPCII 1.44e-01 29 3 62 3 63 AI557158 RPCIII-113020.TJ RPCII 1.44e-01 20 2 612 41 AQ37550 RPCIII-113020.TJ RPCII 1.44e-01 21 93 3 63 AI557158 RPCIII-113020.TJ RPCII 1.44e-01 22 19.3 36 31 R97401 RPSP-2311/4-TR CIT- 22 19.3 36 38 AO375154 RPSP-2311/4-TR CIT- 23 24 AO3050 RPSP-2311/4-TR CIT- 24 46 AO30522 RPSP-2311/4-TR CIT- 25 19.3 36 31 R44531 RPSP-2311/4-TR CIT- 26 19.3 36 31 R44531 RPSP-2311/4-TR CIT- 27 AA505355 RPSP-2311/4-RPSP-2311/4-RPSP-2311/4-RPSP-2311/4-RPSP-2311/4-RPSP-2311/4-RPSP-2311/4	AA754459 1 978N1787 Ric CDNA clone 9 AA754459 92801165 AA754459.1 EST. SATIVA OTYZA SATIVA OTYZA SATIVA CURKATYCHA CONTANTANTANTANTANTANTANTANTANTANTANTANTAN	Contact: Eun M.Y. Department of Cytogenetics Department of Cytogenetics National Inst. of Agri. Sci. and Tech, RDA Suwon, Kyungaldo, Korea Tel: 82 331 290 0307 Fax: 82 331 290 0307 Email: myeun@sun20.asti.re.kr Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji University, Yongin, Korea 449 728 bhnahm@bioserver.myongji.ac.kr Seq primer: M13 Reverse Primer. 1252 Location/Qualifiers Location/Qualifiers Location/Gualifiers Location/Gualifiers
44mmmmmmmmmmmmmmmmmmmmaaaaaaaaaaaaaaaa	AA7544 97SN17 CDNA C AA7544 228011 AA7544 BEST. EST. EVAT. BURATY POACCE 1 (ba Nahm, E Kim, W. Lee, M.	Contac Depart Nation Suwon, Tel: 8 Fax: 8 Fax: 8 Submit Univer
		FEATURES

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/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhOI: Directional cDNA library inserted into lambda ZAPII vector at 5'end with EcoRI and 3' end with Xho I site." /db_xref="taxon:4530"
                                                                                                                  /clone="97SN1787"
/clone=lb="Rice Immature Seed Lambda ZAPII cDNA Library"
/fissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF034173 2275 bp mRNA EST 30-MAR-1998
AF034173 Human mRNA (Tripodis and Ragoussis) Homo sapiens cDNA
Clone ntcon2 contig, mRNA sequence.
AF034173
                                                                                                                                                                                                                                                                                                                                                                          58 VNWSTMTWGTVNWBNVSGDWHYWBVBNTKVDVGNHTRCSRWRBVTRMAHYHDYTNCBBYN 117
                                                                                                                                                                                                                                                                                                                                                                                                    ::| |: :::| |: :: | |::: ::: :: :: :: | |: ::::| ::: | 99 AATTTGTTGTTTAATCTTAATTAGAACTATTTTTT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota, Atazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2275)
Triphodis,v. and Ragoussis,v.
Triphodis,v. and Ragoussis,v.
Generation of a transcription map in the region immediately centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
On Jan 19, 1998 this sequence version replaced g1:2045115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="ntcon2 contig"
/clone_lib="Human mRNA (Tripodis and Ragoussis)"
619 c 470 g 500 +
                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                          Length 252;
                                                                                                                                                                                                                                179 others
                                                                                                                                                                                                                                                                                                                                   41; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Tripodis, Nikos
Division of Medical and Molecular Genetics
Guys Hospital
7th floor, Guy's Tower, London SE1 9RT, UK
Email: nikosénki.nl.
Location/Qualifiers
1. .2275
                                                                                                                                                                                                                                                                                          Score 31; DB 17;
Pred. No. 3.63e-08;
                                                                                                                                                                                                                              35 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism-"Homo sapiens"
/db_xref-"taxon:9606"
/map-"6p21.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1537 YTSTYYKSWSRWYWYTTYTYWYCWCCTSMK 1566
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/cultivar="Milyang23"
                                                                                                                                                                                                                              12 g
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AF034173.1 GI:2707735
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larity 9.5%;
Conservative
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/organism="Oryza sativa"
/cultivar="Milyang23"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional CDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
                  AA754459 252 bp mRNA EST 20-JAN-1998
SYSNIT87 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
CDNA clone 97SN1787, mRNA sequence.
AA754459
                                                                                                                                                                                                     Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
21 c 12 g 35 t 179 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
Fax: 82 311 290 0307
Small: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: MI3 Reverse Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                         Poaceae; Oryza.
1 (bases 1 to 252)
Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,B.P.,
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
                                                                                                                                                                                                                                                                                                                                                               Lee,M.C. and Eun,M.Y.
Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
Unpublished (1998)
On Jan 14, 1998 this sequence version replaced gi:1797457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A1267433 365 bp mRNA EST 17-NOV-1998 aq47e06.xl Stanley Frontal NB pool 2 Homo sapiens cDNA clone IMAGE: 2034082, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 BAMMITSYBCHGNBVWVCVASHGNYMSVHNCIBRGIHCDCKNVNWSIMIWGIVNWBNVSG 75
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Pred. No. 1.97e-06;
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                                                                                                                                  AA754459.1 GI:2801165
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ilarity 12.7%;
Conservative
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                                                                                                                                                                                  Oryza sativa.
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TITLE JOURNAL COMMENT

FEATURES

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/ordeminshmento saptens:
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//ordeminshmento vector: pcR2.1-TOPO (Invitrogen);
//ordeminshmento vector: pcR2.1-TOPO (Invitrogen);
//ordeminshmento vector: pcR2.1-TOPO (Invitrogen);
//ordeminshmento vector respectible value of and older older of primer containing Real and Hindill sites.

Double- stranded cDNA was digested with Real, resulting in blunt ended cDNA of an average 0.1-2 kb in length.

Digested cDNA was split into two sets, one used as is as the driver, the other set was split in half again and each half linked to a different adaptor.

(5'-TCGACCGCCCCCGCCCGCAGGCAGT-3'), to be used as tester.

Subtraction was performed using the Clontech PCR Select CDNA subtraction kit. Pool of two mentally normal males, ages 41 and 53 (S-124, S-141) subtracted by pool of two bipolar males, ages 45 and 50 (S-111, S-128). Tissues were obtained from the Stanley Neuropathology Consortium (www.stanleylab.org). Library constructed and subtracted by Dr. Nancy Johnston [(410) 614-3918, days "Exef"-taxon:9606"
//map="6: 21q"
//map="6: 21q"
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CpG0587A CpIOWAgDNAl Cryptosporidium parvum genomic, genomic survey
sequence.
AQ083705
           1 (bases 1 to 392)
Hiller, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lary, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashU-NCI human_EST Project
                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 378.
Location/Qualifiers
                                                                                                                                                                                                                                            Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2150725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cryptosporidium parvum
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.
1 (bases 1 to 675)
Strong,W.B. and Nelson,R.G.
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/tissue_type="frontal lobe (see description)"
/lab.host="DH10B (phage-resistant)"
58 c 77 g 119 t
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Local Similarity 79.1%; Pred. No. 4.01e-03;
Nes 34; Conservative 0; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .392
/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40UP from Gibco High quality sequence stop: 334.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 365)
Hillier, L., Allen, M. Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Washu NCI human EST Project
Unpublished (1997)
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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/clone_lib="Stanley Frontal NB pool 2"
/tissue_type="frontal lobe (see description)"
/lab_host="DH10B (phage-resistant)"
/ 3 9 106 t
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Pred. No. 4.01e-03;
0; Mismatches 9; Indels
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    .365
    /organism="Homo sapiens"

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21.9%;
Best Local Similarity 79.1%;
Matches 34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
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1 (bases 1 to 356)

S Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C. Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)

Other, GSSs: RPCIII-69M19.TK
Contact: Mark Adams
Contact: Mark Adams
The Institute for Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQ268382 356 bp DNA GSS 26-OCT-1998
RPCII1-69M19.TJ RPCII1 Homo sapiens genomic clone R-69M19, genomic
survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (http://sequence-
www.stanford.edu/group/techdev/shear.htm). The randomly
sheared gDNA was chromatographed on Sephacryl S-400 to
remove any small fragments and DNA eluting in the void
volume was subcloned into an EcoR V-digested, alkaline
phosphatase-treated pBlueScript II (SK-) vector and
transformed into E. coll strain XL2 Blue MRF'.
Recombinant clones from the first plating of the library
were selected for sequence analysis using T3 and T7
                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pBlueScript II (SK-); Site_1: EcoRV; C. parvum (IOWA isolate) genomic DNA was hydrodynamically sheared to produce fragments having a tight size distribution between 2-4 kb by Dr. Yoonne Thorstenson of the Stanford DNA Sequencing and Technology Center
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                                                                                            Depts. of Medicine & Pharmaceutical Chemistry
San Francisco General Hospital-University of California, San
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For clone availability, please contact Pieter de Jong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 25; DB 39; Length 675; Pred. No. 4.01e-03; 0; Mismatches 2; Indels
                                                                                                                                    Francisco
Box 0811, San Francisco, CA 94143-0811, USA
Tel: 415 206 8846
Fax: 415 206 3353
Email: malaria@itsa.ucsf.edu
Seq primer: M13(-21) forward
                                                                                                                                                                                                                                                                                                                                              /organism="Cryptosporidium parvum"/strain="IOWA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="CpIOWAGDNA1"
/lab_host="E. coli XL2 Blue MRF'"
93 c 95 g 216 t
Cryptosporidium parvum GST Project Unpublished (1997)
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                                                                       Contact: Nelson, R. G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 21.9%;
Best Local Similarity 93.1%;
Matches 27; Conservative
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                                                                                                                                                                                                                                                                              Class: shotgun.
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Muscharia;
Eutheria; Nodentiai; Sclurognathi; Muridae; Muschas; Musca, Musca, M., Hilliar, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Schellenberg, K., Mylie, T., Lennon, G., Soares, B., Wilson, R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA764146 359 bp mRNA EST 27-JAN-1998 vv45d06.rl Soares 2NbMT Mus musculus cDNA clone IMAGE:1225355 5', mRNA sequence.
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                                                                                                                                                                                                /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCIII Human Male BAC Library"
/db_xref="GDB:7526418"
/db_xref="taxon:9606"
/clone="R-69M19"
/clone="R-69M19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:650947
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Unpublished (1996)
On Apr 14, 1993 this sequence version replaced g1:693044.
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Washloren University School of MedicineP
4444 Forrest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 356;
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0; Mismatches 11; Indels
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Seg primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 339.
Location/Qualifiers
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                                                                                                                                                                           /organism-"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                           /cell_type="Lymphocytes'
62 c 45 g 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 24;
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1. .356
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                                                                                                                                                                                                                                                                                                                                                         /sex="Male"
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Best Local Similarity 76.1%;
Matches 35; Conservative
                                                                                                    Class: BAC ends
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AU033574.1 GI:3798998
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llarity 76.1%; 1
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(Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

/db_xref="taxon:10090"
/clone="InAGE:1225355"
/clone="InAGE:1225355"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryotes, Dictyosteliida, Dictyostelium.

[ (bases 1 to 423)

Morlo,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M.,
Yoshino,R., Mitra,B.N., Pi,M., Sato,T., Takenoto,K., Yasukawa,H.,
Williams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y.
The Dictyostelium developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage of
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AU039222 423 bp mRNA EST 29-WAR-1999
AU039222 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium
discoideum cDNA clone SLH180, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                Gaps
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Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT = 'Dictyostelium discoideum cDNA project in Japan'.
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                                                                                                                                                                                                                                                                             Length 359;
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                                                                                                                                                                                                                                                                                                            0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                          7 GATGATAAATAAATTTCACTAAGAGCAATGAAAAAATTAAC 52
                                                                                                                                                                                                                                                                                                                                                                3 GATGATATTAAAAAACTTTCAGAAAAAGAATTGCAAAAAATAAAC 48
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Institute of Biological Sciences
University of Tsukuba
                                                                                                                                                             /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Res. 5 (6), 335-340 (1998)
99156227
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57 c 44
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21.1%;
Best Local Similarity 76.1%;
Matches 35; Conservative
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21.1%;
Best Local Similarity 71.4%;
Matches 40; Conservative
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AQ268460 434 bp DNA GSS 26-OCT-1998
RPCIII-74G21 TJ RPCIII Homo sapiens genomic clone R-74G21, genomic
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1 (bases 1 to 434)
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C. Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mdadams@tigr.org
For clone availability, please contact Pieter de Jong
For clone availability, please contact Pieter de Jong
For clone availability, please contact Pieter de Jong
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: SP6
Class: BAC ends.
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/organism="Homo sapiens"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
/db_xref="CBB:7528196"
/clone="R74G21"
/sex="Male"
/sex="Male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        388 IGGATAAAGATTAGATTTAGAGTATGAATTAAATTAGAAATATCTC 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 TGGGTAAAAATTGTTTAATGTTATGAATAAAAATTAGAACTATTTC 62
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Pred. No. 2.45e-02;
0; Mismatches 11;
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Dictyostellum discoideum
Ekaryota, Dictyostellida; Dictyostellum.
1 (bases 1 to 435)
Yoshino,R., Morio,T. and Tanaka,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_type="Lymphocytes"
74 c 89 g 12
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Institute of Biological Sciences
University of Tsukuba
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328 TATTGTCTGCAATTCTTTGAATGAAAGTTTTTTA 361
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 530)
Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.
Use of BAC End Sequences from Library RPCIII for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: hbe@tigr.org

for clone availability, please contact Pieter de Jong

(pieter@dejong mac.buffalo.edu). Clones may be purchased from

Research Genetics (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.

Seq primer: SP6

Class: BAC ends.
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                                                                                              /strain="XX4"
/db_xref="taxon:44689"
/clone="SLB183"
/clone="SLB183"
/clone="SLB183"
/dev_stage="slug"
62 c 43 g 148 t
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RPCIII Human Male BAC Library"

/db_xxef="cDB:7543600"

/db_xxef="taxon:9606"

/clone="R-114117"

/clone=lib="RPCIII"
                                                                                                                                                                                                                                                                                                                                                                                                                        AQ344881 530 bp DNA GSS 21-JAN-1999
RPCI11-114117.TJ RPCI11 HOMO Sapiens genomic clone R-114117,
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                                                                                                                                                                                                                                                                                                                    Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT - Dictyostelium discoideum cDNA project in Japan.
Location/Qualifiers
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Other_GSSs: RPCIII-114117.TV
Other_GSSs: RPCIII-114117.TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
1911: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41; Length 530;
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Pred. No. 2.45e-02;
....ma+ches 5; Indels
 3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
                                                                                     /organism="Dictyostelium discoideum"
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1. .530
/organism="Homo sapiens"
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67 c 108 g 13
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AQ344881
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ilarity 85.3%;
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ilarity 71.4%;
Conservative
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Best Local Similarity
Matches 40; Conserv
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Best Local Similarity
Matches 29; Conser
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Tel: (301) 496-1550
Email: Robert_Strausberg@nlh.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NII-GAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/organism="Ungan: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.85 kb. Life Technologies catalog #:
11539-012"
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                                                                                                                                             AI570972 133 bp mRNA EST 29-MAR-1999 to24q03.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2180020 3' similar to contains element LTR3 repetitive element ;, mRNA
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1 (bases 1 to 133)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)

On Mar 20, 1998 this sequence version replaced gi:2980227.
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WCCE3650.MIF Schistosoma mansoni, cercariae Schistosoma mansoni
CDNA clone SM3650C 3' end, mRNA sequence.
AA999637
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/clone="IMAGE:2180020"
/clone_lib="NCI_CGAP_Ut2"
/tissue_type="moderately-differentiated endometrial
adenocarcinoma, 3 pooled tumors"
/lab_bost="DH108"
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45 TATTTTTGCAATTCTTTTTCTGAAAGTTTTTTA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: -40UP from Glbco
High quality sequence stop: 103.
Location/Qualifiers
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AI570972.1 GI:4534346
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Schistosoma mansoni.
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Best Local Similarity
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SOURCE
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. Wed.Sep 15 12:54:07 1999

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234 ATAAAATTTAAAAATTTAAAAAAAAAGGTTTGCAAAATGTAA 276
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Eutheria; Princes; Erichae, F.D., Fuldner, R.D., Fuldner, R.D., Man-Mai, C., Blake, J.A., Brandon, R.C., Man-Mai, C., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fitzperald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodk, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Merley, J.G., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R., Mononald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.T., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
                                                                          1 (bases 1 to 252)
Santos, T., Azevedo, V., Marotta, G.B., Santos, R.L., Fonseca, S.J.,
Ortega, J.M., Rabelo, E.M.L., Saber, M., Abdel-Hamid, H., Ridgers, I.L.,
Johnston, D.A., Fernandez, M., Rollinson, D., Franco, G.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Avenida Antonio Carlos 6627, Belo Horizonte, MG, Brazil, 31270-010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Schistosoma mansoni"
/strain="NmRI"
/strain="NmRI"
/note="Vector: pBlueScript SK; Site_1: XhoI; Site_2:
ECORI: mRNA was extracted from cercariae and the library
was constructed and excised according to the
manufacturers instructions (Uni-Zap XR vector,
Stratagene)"
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EST38687 Embryo, 9 week Homo sapiens cDNA 5' end, mRNA sequence.
AA334468
                                                                                                                                                                                                                                                                                                                                                                                                                                         Instituto de Ciencias Biologicas, Universidade Federal de Minas
                                                                                                                                                                                                          Analysis...
Cercariae using EST approach
Unpublished (1998)
On Jan 17, 1998 this sequence version replaced g1:2043380.
                         Eukaryota, Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
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Pred. No. 1.44e-01;
0; Mismatches 15; Indels 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                            Contact: Santos, T.M. and Pena, S.D.J.
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t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: (5531)4415611
Fax: (5531)4415409
Email: santostm@mono.icb.ufmg.br
Seq primer: M13 Forward.
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/lab_host="DH5alpha"
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Best Local Similarity 71.7%;
Matches 38; Conservative
Schistosoma mansoni
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SOURCE
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He,W.W., Hu,J.S., Greene,J.W., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Melssner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wingy,J., Xu,C., Yu,G.L., Ruben,S.M., Dilliton,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
Information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse
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                                                                                                                                                                                                                                                                                            On Apr 14, 1993 this sequence version replaced gi:716849. Other_ESTS: THC178342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 others
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/db_xref="taxon:9606"
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/dev_stage="embryo, 9 wks"
/dev_stage="embryo, 9 wks"
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/organism="Homo sapiens"
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